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GenCore version 5.1.6 .
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OM nucleic - nucleic search, using sw model	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:*.  1: gb_ba:* 2: gb_ing:* 3: gb_on:* 4: gb_on:* 5: gb_ov:* 6: gb_pt:* 7: gb_pt:* 10: gb_pt:* 11: gb_rs:* 11: gb_rs:* 12: qb_gr:*
	Title: Perfect score: 2074 Sequence: 1 ctgcagcaagttacttaatgacaagactccttcagccaac 2074 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters: 5777422 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	taatg kt 1.0 548j3386 resic hosen paramete summaries
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SUMMARIES

Result	Score	Query	Length	BG	QI.		Descript	ion
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21-JUN-2002 10, Submitted (21-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 23, 2002 this sequence version replaced gi:12191663.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. AL365434 linear PRI Human DNA linear PRI Human DNA sequence from clone RP11-236B18 on chromosome complete sequence. AL365434.13 GI:21540024 (bases 1 to 158357) Homo sapiens (human) lrect Submission Homo sapiens Bird, C AL365434/c LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL COMMENT

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSROT; Tr., TREMBL; Wp., WORNPEP, information the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10. Constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/HGFC/hr10

RPII-236Bls is from the library RPCI:11:1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality date (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers This sequence was finished as follows unless otherwise noted: all Length 158357; Center: Wellcome Trust Sanger Institute /clone="RP11-236B18" /clone lib="RPCI-11.1" a 32356 c 32839 g 46204 Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" --- Genome Center chromosome="10" 1. .158357 Query Match source BASE COUNT ORIGIN

1443 1383 1323 , 1322 GGCCTGGAACAAAAGGCATACGAAATGGTAGAAAAGTGTCCATGACTACTTCTGACTT 1263 119 179 239 59 1 CTGCAGCAAGTTACTTAATGTTT-TTTGCCTCAGCATCCTCTCTGTAAAATGAGAGCATT AGTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAA AGATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAA 180 GCCTGGAACAAAAGGCATACGAAATGGTAGAAAAGTGTCCATGACTACTTCTGACTT Gaps 10; Indels 10; 67.3%; Score 1395; DB 9; 98.4%; Pred. No. 7.2e-307; 4; Mismatches Best Local Similarity 98.4 Matches 1479; Conservative 09 240 g qq ò ò

1262 AGATGAAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAA 1203 g g ð 8

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Homo sapiens chromosome 10 clone RP11-236B18, WORKING DRAFT SEQUENCE, 17 unordered pieces.
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11 (bases 1 to 160350)
Waterston,R.H.
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Submitted (13-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:9665205.
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HOMO sapiens (human)
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	240 AGATGAAGAGCCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAA 299 	300 AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTG 359 	360 TGAAACATTCCATATATTAAAAATAAATAATAAGAGAAAAGGAAAAAGAAAAAA	420 GAAAATAGTGATAGCTGTGTCCATCTCAAAGAAAGCCCAGGAGATTTCCTTTATTTA	478 CCCCTTTAAGATAGAATATTAGGAGACCGGAACATATGATACAGGAGGTACTGGGAGGG 537 	538 TCCCTCTTTGTCAAUGTTTTGTCTTGGGGGGGGGGTCGATGTCTTCTCAAAGTTTCAGA 597 	598 AACACCATCCACTGACCATTCAAGGGGCAAGAGGAAATGGCAGCCACATTTGTTG 657 	658 ATTGGGTGAGTTTGGGGAGAAATAGACACACAAAGGTCAAACATAACTTCCTAATTAACA 717 	718 CTTCCCTCCATTCAAATTCCCTTCTCCCATTCTTCTCCTGTCTTTTACTSAKARAA 777 	778 CCCAGTITITCCTGAAACTAFAAAAATACCCCCAGTATGTTTACATAATTTACACCTCAA 837 	838 AGATTAGAAACCAGNAATAGAGACC-TTTTCAACCCTTCCGGAAGCAAAGTGCATTATCC 896	897 CICCAGCCACGIGICICAAATCIIGATGCAICAGAATCAICIGGGTGCTITKAAAIICAA 956 	957 GATGATTACCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGG-CCAGGGAT 1015 		1076 CTCAATGACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATAT 1135 	ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 119	1196 CCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAATGTTGGGATTACAGGTGTAAGC 1255
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* 113398 113497: gap of unknown length * 113498 141732: contig of 28235 bp in length * 141733 141832: gap of unknown length * 141833 143187: contig of 1355 bp in length * 143188 143287: gap of unknown length * 143288 144942: contig of 1655 bp in length	144943 145042: gap of unknown length 145043 147286: contrig of 2244 bp in 1 147287 147286: gap of unknown length 147387 150852: contrig of 3466 bp in 1	150853 150952: gap of unknown 150953 153550: contig of 2598 153551 153650: gap of unknown 153651 15757: contig of 3607 15757: contig of 3607 15757:	15/258 15/359 15/359 15/358 16/350: contig of 2993 Location/Qualifiers 1160350	/organisme"idomo sapiens" /mol_type="genomic DNA" /db_xref="texon:606" /chromosome="10"	/clone="RP11-236BlB" nisc_feature 1. 2326 /note="assembly_name:Contigl0" misc_feature 24277519	/note="assembly_name:Contig11" /note="assembly_name:Contig12" misc_feature 15387. 23050	/note="assembly_name:Contigl3" 215133663 /note="assembly_name:Contigl4" misc_feature 3376450133	/note="assembly_name:Contigl5" %	/note="assembly_name:Contig17" misc_feature 88234".113397 note="assembly_name:Contig18" misc_feature 113498141732	/note="assembly" name:Contigly" misc_feature 141833	/note="assembly_name:Contig4"   145043. 147286   note="assembly_name:Contig5"   misc_feature	/note="assembly_name:Contig6" misc_feature 150953153550 nisc_feature 153651157257	/note="assembly_name:Contig8" misc_feature 157358160350 /note="assembly_name:Contig9" BASE COUNT 47390 a 32724 c 33135 g 45498 t 1603 others	Query Match Query Match Best Local Similarity 92.0%; Promoter No. 7.2e-307; Matches 1482; Conservative 4; Mismatches 115; Indels 10; Gaps 7;	1 CTGCAGCAAGTTACTTAATGTTT-TTTGCCTCAGCATCCTCTGTAAAATGAGAGCATT 59	60 AGTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAA	

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/evidence=not_experimental
join(391. .472_3273. .3328,3962. .4018,4428. .4502,7467. .7538,
14216. .14306,23179. .23295,23858. .23887,24284. .24321,
24717. .24796,28974. .29083)
/gene="bA320F15.1"
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/note="match: proteins: Tr:P78346 Tr:O88796"
/codon: grart=1
/codon: grart=1
/evidence=not_experimenta1
/product="ba32015.1.1 (ribonuclease P (30kD) (RPP30))"
/product="ba32015.1 (ribonuclease P (30kD) (RPP30))"
/product="ba32015.1 (ribonucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2349. .2482

/note="L2 repeat: matches 2557. .2696 of consensus"

2939. .3167

/note="Mix repeat: matches 13. .262 of consensus"

/note="match: GSS: Em:AQ626500"

/note="match: GSS: Em:AQ626500"

/note="match: GSS: Em:AQ626500"

/gene="bA320F15.1"

/gene="bA320F15.1"
                                    IMPORTANT: This sequence is not the entire insert of clone RP11-320F15 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-236B18 is at 5012 in this sequence. The true right end of clone RP11-103A2 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jóin(120. 472,3273. 3328,3962. 4018,4428. 4502,7467. 14216. 14302,23179. 22295,23858. 23887,24284. 24321, 24717. 24796,28974. 29381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="halloris.1.1 (ribonuclease P (30kD) (RPP30))"
/note="march: cDNAs: Em:U77665 Em:AK004137 Em:U95123
match: EST9: Em:BE57269 Em:BE378859 Em:BE137893
Em:AA920575 Em:BG106620 Em:BF681617 Em:BF248001
Em:BF031745 Em:AA854455 Em:A1359795"
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/note="L2 repeat: matches 2459. .2502 of consensus"
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note="MIR_repeat: matches 30. .132 of consensus"
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note="match: ESTs: Em:AW939965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11.2"
complement(1. .98)
/note="match: GSS: Em:AQ670367"
complement(1. .97)
/note="match: GSS: Em:AQ544636"
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                                                                                                                                                                                                                                                                                                                      .. .50111
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="RP11-320F15"
                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note="match: STS:
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/gene="bA320F15.1"
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gene="bA320F15.1"
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/gene="bA320F15.1"
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                                                                                                                                                                                                                                                                             FEATURES
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL: Sw.; SWISSPROT; Tr., TREMBL: WORMPEP; Information on the WORMPEP there. All the segments.
                                                                                                                                                                                                                                                                             113800 CCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGC 113741
                                                                                                                  1433 TAATGATGGTAAGGTGGCATGTCATGGGGCCTATTTAG-CCCAGACATCACTCCAAAGAA 1491
                                                                                                                                                                                                                                                                                                                                                                                           1376 TA---ATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTA 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1492 TTCCAAACAGATATAGACAAGTGCCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTA 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALS90622 50111 bp DNA linear PRI 19-SEP-2001 Minan DNA sequence from clone RP11-320F15 on chromosome 10. Contains the gene for ribonuclease P 30kD subunit, the gene for an unclear protein similar to CARP, ESTS, STSS and GSSS, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/RGP/Chr10 RP11-320F15 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50111)
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                                                                             CACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATT
                                                                                                                                                                                                                                    1316 TTGAAGTAAAAATGCTCCAATTATTATGCTGTTTTTAGAACACGGTAAGCATGTCATGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1552 CCCAGGGAATAGGATGTCCTGGGACAAGTTTCCCCTAAGTGAAGTGTTGAT 1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARP; . ribonuclease P.
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                                                                                                                                                                                                                                                                                                                                                                                                           1456 ATGGGGCCTATTTAG-CCCAGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTG
                                                                                                                                                                                                                                                                                                      1515 CCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTACCCCAGGGAATAGGATGTCCTGGG
                                                                                                                                                                                                                                                                                                                    1575 ACAAGTTTCCCCTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAAGATATTACTGGGGG
                                                                                                                                                                                                                                                                                                                                                                      1695 AAAAAGGGCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCCTGACTCTTGACAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1935 GTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCCAGCTATATAAGCTGA
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                                                    /note="L2 repeat: matches 2636. .2710 of consensus" 29149. .29154
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complement (25417. .25863)
/note="match: GSS: Em:AQ712354"
26204. .26603
/note="LIMA2 repeat: matches 5888. .6302
                                                                                                                                                Length
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                                                                                                                                             Query Match 32.1%; Score 664.8; DB 9; Best Local Similarity 99.6%; Pred. No. 9.2e-141; Matches 677; Conservative 0; Mismatches 2;
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Sequence 1 from Patent WO0246220.
AX468603
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29166
/gene="bA320F15.1"
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Mus musculus
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join(23179. 23295,23858. 23887,24284. .24321,24717. .24796,
28974. .29072,30647. .30748,31596. .31680,33706. .34469)
/gene="bA320F15.1.3"
/product="bA320F15.1.3"
/product="bA320F15.1.3"
/note="match: EST8: Em:BE567341 Em:AI292002 Em:BF684192
Em:BF435407 Em:AI740881 Em:AA651912 Em:BF438915"
/evidence=not_experimental
/gene="bA320F15.1"
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complement(join(24284. .24321,24724. .24796,28974. .29240))
/note="match: STS: Em:G24365"
                                                                                                                                                                                                                                                                                                                                                                                                                                             9601. .9741
/note="MIR repeat: matches 76. .212 of consensus"
10798. .11076
/note="Ally repeat: matches 1. .291 of consensus"
11086. .11219
/note="FLAM C repeat: matches 1. .129 of consensus"
11319. .11491
/note="MIR repeat: matches 3. .189 of consensus"
11928. .11984 repeat: matches 1743. .1801 of consensus"
11955. .13817
/note="L2 repeat: matches 2684. .2749 of consensus"
13755. .13817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //gene="bA320F15.1"
/note="match: GSS: Em:B53566"
25321. .25458
/note="FLAM_C repeat: matches 1. .133 of consensus"
                                                                                                                               /note="L2 repeat: matches 1200, .1808 of consensus"
8884. .7196
/note="AluJb repeat: matches 1. .312 of consensus"
                            .2732 of consensus"
                                                       consensus,
                                                                              .1971 of consensus"
                                                                                                        .293 of consensus"
                                                                                                                                                                                                                                                   8243. .8404
/note="2 copies 81 mer 81% conserved"
8445. .8841
/note="HY1 repeat: matches 16. .112 of consensus"
8542. .8583
/note="HY1 repeat: matches 1. .42 of consensus"
                                                    .2478 of
    4928. .5102

4928. .5102

"note="L2 reno?"
                               ...ue="L2 repeat: matches 2299.
5257. .5439
"note="L2 rene"*
                                                                                           5440. .5721
/note=#AluSx repeat: matches 7.
5722. .6237
/note="L2 repeat: matches 1200.
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24561. .24956
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2191 TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCCAGCCCTAGCTATAA-CGGGCTG 2249
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                                                                                                                                                                                                                                                                                                                                                                                                       1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1349 TTAGAACACGGTAAGCATGTCATGTGCTA---ATGGCCAGTGACATCATAAAAGAAAGT 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1658 GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT 1717
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                          Sequences upstream of the carp gene, vectors containing them and
uses thereof
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                                                                                                                                  The University of
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                                                                                                                                                                                                                                                                                                                            Score 367.8; DB 6; Length 2358;
Pred. No. 3.6e-73;
0; Mismatches 162; Indels 22;
                                                                                                            Patent: WO 0246220-A 1 13-JUN-2002;
Aventis Pharma S.A. (FR); The Regents of The Unive
California at San Diego (US); Benoit, Patrick (FR)
Location/Qualifiers
                                                        Schwartz, B., Branellec, D. and Chien, K.
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76.48;
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 61126: contig of 61126 bp in length

* 61127 142205: contig of 81676 bp in length.

Location/Qualifiers
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                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------------- Project_Information
Center project name: 1.22236
Center clone name: 211_P_24
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Pred. No. 3.2e-73;
0; Mismatches 162; Indels
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30899 c 29987 g 40473 t 167 others
                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-211P24"
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Best Local Similarity 76.4%;
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23101653.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.chc.ltm.cad/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, X.-Z., Sozelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, R., Wei, X., White, F., Wailliams, G., Willson, R., Warren, R., Wei, X., Woon, L., Yoon, L., Yo, F., Zhang, J., Zhou, J., Yaku, S., Yen, J., Yoon, L., Yoo, L., Yo, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
L. Unpublished
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NOTE: This is a "working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Center project name: GNAG
Center clone name: CH230-140118
Center clone name: CH230-140118
Assembly program: Phrap; version 0.990329
Consensus quality: 217436 bases at least Q40
Consensus quality: 217436 bases at least Q20
Consensus quality: 217436 bases at least Q20
Estimated insert size: 214300; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium.
Direct Submission
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TITLE
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AUTHORS
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1702 GCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCTGACTCTTGACAAATAGGATGA 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1349 TTAGAACACGGTAAGCATGTCATGTGCTAATGGCCAGTGACATCATAAAAGAAAAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141497 TTAGAGCAC----ATGCCATGCACTAATTATGGCCAGTGACACCATAAAGTAAAAGTGCA
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244771: contig of 1611 bp in length
24872 2284871: gap of unknown length
24872 225886: contig of 1015 bp in length
2587 225886: contig of 1015 bp in length
15987 225286: gap of unknown length
15987 228280: gap of unknown length
181 225840: contig of 1360 bp in length
10. cation/Qualifiers
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                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-140118"
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213542. .215467
/note="wgs_end_extension
clone_end:T7"
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/note="wgs_end_extension
clone_end:T7"
complement(7251. .8156)
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lone_end:\overline{T7"
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clone_end:T7
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/note="clone_boundary
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Submitted (14-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 14, 2002 this sequence version replaced gi:22855482.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each connig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Trajos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Walse, R., Waltson, E., Waldron, L., Walker, B., Wang, J., Wright, D., Walghe, R., Weczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wul, Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zako, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Wainstock, G. and Gibbs, R.A.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* sons known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley,K.C.
Direct Submission
Submitted (11-007-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Center clone name: GGO30-26A2
Center clone name: CH230-26A2
Assembly program: Phrap: version 0.990329
Consensus quality: 222569 bases at least Q40
Consensus quality: 226638 bases at least Q30
Consensus quality: 22427 bases at least Q20
Estimated insert size: 233018; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236546: contig of 236546 bp in length 236547 236446: gap of unknown length 236447 23844: contig of 1698 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                            142082 TTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTATATAAAG-AGGCTGGGGT 142140
        141847 GCAGCGATGTGGTGCAATATGAACAGGCAGCTGTCCCTGGCTTCCCGATAAGTAGGATGA 141906
                                                                                                                                                                                                                                                                                    ATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCTCTTCAGCTTCCCAGACACTG 1881
                                                                                    1762 CTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTTCCTG 1821
                                                                                                                                                                                                                                                                                                                                                                                                AGTCTGGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGCGGGAGTGTTAC 1941
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*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142141 GGAGGGCTCCACAGGGCCAGCTCCAGGGGTTCAGCCACAAGAGGGGAAAAACATAGA 142197
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002 GGAGGGGCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAAAAAATAAAA 2057
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HTG; HTGS_PHASE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Musinae; Musinae; Musinae; Musinae; Li (bases 1 to 723)

Maeda T., Sepulveda, J., Chen, H.H. and Stewart, A.F.R.

alphal-Adrenergic activation of the cardiac ankyrin repeat protein gene in cardiac myocytes

I. Gene 297 (1-2), 1-9 (2002)

E. Maeda, T., Sepulveda, J. and Stewart, A.F.R.

Direct Submission

Submitted (19-JAN-2002) Cardiovascular Institute, University of Pittsburgh, 200 Lothrop Street, Pittsburgh, PA 15213, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1767 ATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTTCCTGATTCA 1826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cardiac ankyrin repeat protein"
721. .>723
/gene="Carp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon start=1
/product="cardiac ankyrin repeat protein"
/protein id="AAL85342.1"
/db_xref="GI:19110907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.4%; Score 340.8; DB 10; Length ilarity 74.0%; Pred. No. 5.2e-67; Conservative 0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains promoter and 5' UTR' <721. >723 /gene="Carp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                        1. .723
/organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="FVB"
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'gene="Carp"
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  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27182 TTACTGAATGCTTTCAATTTCTCATAATGATGGTAAGGTGGCGTGTCATGGGGCCATTTT 27241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27242 AGCCCTGGACATCACTCCAGAGAATTCTGAACAGATATAGACAAGTGTCACCAAGACCCA 27301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27302 -----CTTCCCCCCGGGCTGTTTATTCCCAGGAATAGGATGTCCCAAAGCAACACTTCCA 27356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17711 TIGGCTTCCCAGGCTGGAAGATTATCTCACCCAGTCCTAGCTATATAAG-AGGCTGGGGT 27769
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                                                                                                                                                                                                                                                                                                                                                                                          1409 TTACTGAATGCTTTCAATGTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTATTT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1469 AGCCC-AGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGGCCCA 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1528 GATCCCTTCCCCTCAGGCTGTTTA-CCCAGGGAATAGGATGTCCTGGGACAAGTTTCCC- 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1586 --CTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAAGATATTACTGGGGGGTGTGATATG 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1644 TAGGGCATCTACATTTTCTTGATAGGTAGTCATATGAAAGCTGACAAAGGA--AAAAAGG 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1702 GCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCCTGACTCTTGACAAATAGGATGA 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1762 CTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTTCCTG 1821
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                                                                                                                                                                                                                        1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT
                                                                                                                                                                                                                                                                                                         1349 TTAGAACACGGTAAGCATGTCATGTGCTAATGGCCAGTGACATCATAAAAGAAAAGTGCA
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                                                                                                                                                                                     Gaps
                                                                                                                                                                                     26;
                                                                                                                                        Query Match 17.6%; Score 365; DB 2; Length 238344; Best Local Similarity 77.3%; Pred. No. 1.4e-72; Matches 601; Conservative 0; Mismatches 150; Indels 26;
                                                                                 6855 others
                                                       /note="wgs_contig"
47381 c 49225 g 71429 t
db_xref="taxon:10116"
            /clone="CH230-26A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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LOCUS DEFINITION

RESULT 10 AF478692

ACCESSION VERSION KEYWORDS SOURCE

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(250). .(1206)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
a 378 c 460 g 471
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                                                                               TITLE
JOURNAL
                                        REFERENCE
AUTHORS
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HSRNACINP
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                                                                    GGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGCGGGGGTGTTACTTCGG
                                                                                                        1947 TICCCAGGIIGGAAGAIIAICICACCCGGCCCCAGCIAIAAAGCIGACCGGIGIGGGG
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1827 CATATICAGCAGGGITAGCTIGICCICCCTCCCTCCTTCAGCTICCCAGACACIGAGICI
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Pred. No. 2.3e-41;
0; Mismatches 5; Indels
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Novel target genes for diseases of the heart
Patent: WO 0192567-A 19 06-DEC-2001;
Medigene AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                          DNA
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
a 378 c 460 g 471
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Sequence 19 from Patent WO0192567.
AX322775
AX322775.1 GI:18093755
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Best Local Similarity 97.6%;
Matches 242; Conservative
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Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dassa 1 to 1901)

1. (Dassa 1 to 1901)

2. Nojima, H., Yoshisue, H., Obayashi, M., Ota, T., Kawabata, A., Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

2. Shear stress-responsive DNAs

2. Patent: WO 012547-A 37 12-APR-2001;

KYOWA HAKKO KOGYO CO LTD, HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA

SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO

OS HOmo sapiens (human)

PN WO 0125427-A/37

PD 12-APR-2001

PR 02-OCT-2000 WO 2000JP006840

PR 01-OCT-1999 JP 99P 280976

PR HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI
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PI KAZUHIRO SAWKRADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA,

PI SUMIO SUGANO
C 122115/12, C07X14/435, C07X16/18, C12221/02, C1221/68, A61X38/00,

PC A61X48/00, A61P9/10, G01N33/53,

C A61X48/00, A61P9/10, G01N34/54,

C A61X48/00, A61P9/
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Butheria, Primates, Catarrhini, Hominidae,
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AUTHORS
TITLE
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1828 ATATTCAGCAGGGTTAGCTTGT-CCTCCCTCCTTCAGCTTCCCAGACACTGAGTCT 1886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prepared with primer pairs provided by Sandoz, derived from X83703
-- Washington University/Merck EST sequence.
Location/Qualifiers
1. .1901
/organism="Homo sapiens"
/mol_type="genomic DNA"
                                            Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                    seconds
seconds
                                                                                                                                                                                                                                                                                                                                                               Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                             Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
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62 degrees C for 23 si
72 degrees C for 30 si
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Perkin Elmer 9600
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each 200 uM
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Primer B: CCAGATGGATGATCATGAAGG
STS size: 222
PCR Profile:
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378 c 460 g 4
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                                          Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1901)
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Total Vol:
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Polymerization:
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           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cycles:
                                                                                             Myers, R.M.
Unpublished (1996)
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Tris-HCl:
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Matches 242; Conservative
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primer_bind
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                                                                                                     Direct Submission
Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland
Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La
Roche, Nutley, NJ 07110, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1828 ATATTCAGCAGGGTTAGCTTGT-CCTCCCCTCCTTCAGCTTCCCAGACACTGAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cytokine-inducible expression"
nuclear protein from human endothelial cells J. Biol. Chem. 270 (17), 10236-10245 (1995) 95247734
                                                                                                                                                                                                                                                                                                                                                                                                 /note="nuclear localization signal"
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2 (bases 1 to 1901)
Chu, W.
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Gaps

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LSTALHVAVRTGHYECABHLIACEADLNAKDREGDTPLHDAVRLNRYKMIRLLIMYGA
DLTIKNSAGKTPMYLLAVRAIPSLKENSYKTSRIATF"
391 c 479 g 447 t
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                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha; Leporidae, Oryctolagus.

1 (bases 1 to 1940)
Aihara, Y., Kurabayashi, M., Arai, M., Kedes, L. and Nagai, R.
Molecular cloning of rabbit CARP cDNA and its regulated expression
in adriamycin-cardiomyopathy
Biochim. Biophys. Acta 1447 (2-3), 318-324 (1999)
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Pred. No. 1.3e-24;
0; Mismatches 31; Indels 2;
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Oryccolagus cuniculus CARP mRNA, complete cds.
AF131883
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Location/Qualifiers
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Best Local Similarity 84.9%;
Matches 185; Conservative
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Aihara, Y.
Direct Submission
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Search completed: November 18, 2003, 04:22:10 Job time : 7557.42 secs

Human immune/haema Genomic sequence # Human immune/haema Human immune/haema Human immune/haema Human nervous syst

Human

Human immune/haema Human immune/haema Human musculoskele Chuman conding nove Human cDNA differe Human TBC-1 partia

Genomic sequence #
Human immune/haema
Human digestive sy
Human nervous syst.
Human immune/haema

AA250905 AAS42003 AAK87230 AAK90644 ABA16110 ABK80063 AAK85377 AAK85378

immune/haema immune/haema immune/haema Human autoimmune d Human secreted pro Human musculoskele

Human

Human

AAK65595 AAK65596 AAK65597

ABX56555 AAC81712

ABQ77794 AAK65971 ABS69895

Run on:

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Cardiac ankyrin repeat protein; CARP; cardiant; immunosuppressive; antiinflammatory; gene therapy; antisense gene therapy; human; ds.
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(REGC ) UNIV CALIFORNIA.
(BENO/) BENOIT P.
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  Murine cardiac ank
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Human shear stress
Human CAA58676 pro
Human DNA sequence
Differentially exp
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Mouse CARP protein
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Result

Human immune/haema Human cDNA differe Human D-amino acid cDNA encoding nove Human immune/haema

ALIGNMENTS

New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells

2; 48pp; English Claim 5; Fig

The invention relates to a polymucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin (Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament of intended for the treatment of cardiac insufficiancy, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a correcting muscle contractility, cardiac hypertrophy, cardiac or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility. (IIb) is useful for expressing a gene of the rapequence in vivo, by isolating (IID) and introducing (IID) in the cardiac tissue, under conditions so that the gene of interest is carpersmental, therapeutic and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating creaming correcting muscles for their activity on the regulatory sequences of the gene of concenting correcting molecules for their activity on the regulatory sequences of the gene of concenting the CARP protein. The present sequence represents the DNA framment unstream of the constitute models for sevents and concention of a human CARP protein. fragment upstream of the coding sequence of a human CARP protein. 

Sequence 2074 BP; 612 A; 469 C; 416 G; 572 T; 5 other;

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540 120 180 300 300 360 360 420 420 480 480 541 CTCTTTGTCAATGTTTTGTCTTGGGGTGGGGAGTCGATGTCTTCTCAAAGTTTCAGAAAC 600 9 9 GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAAA GATGAAGAGCCAATGAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAA ATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACAAATTTGT GAAACATTCCATATATTAAAATAAATAAATAATAAAGAGAAAAAGGAAAAAGG CCTTTAAGATAGAATATTAGGAGACCGGAACATATGATACAGGAGGTACTGGGAGGGTCC crecaecaagrractraarerrrrrreccrcaecarccrcrcraaaareaegagarra GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAAA GCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAGTGTCCATGACTACTTCTGACTTA GCCTGGAACAAAAGGCATACGAAATGGTAGAAAAGTGTCCATGACTACTTCTGACTTA GATGAAGAGCCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAA ATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGT GAAACATTCCATATAAAAATAAATAAATAATAAAGAGAAAAGGAAAAAATTAAAAG certitaagatagatatitaggagaccggaacatatgatacaggaggtactggaggggcc CTGCAGCAAGTTACTTAATGTTTTTTGCCTCAGCATCCTCTCTGTAAAATGAGAGCATTA Gaps DB 24; Length 2074; ö 0; Indels 99.9%; Sco... 100.0%; Pred. No. v, ... 0; Mismatches Conservative Query Match Best Local Similarity Matches 2074; Conserv 121 181 241 61 61 121 181 301 301 361 361 421 421 481 481

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                                                           New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac
                               GCCCTCTCACATTCTTCCTCATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCC
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thended for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of [1] is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac therapeutic interest in vivo, by isolating [11b] and introducing [11b] in the cardiac tissue, under conditions so that the gene of interest is expressed. [1], the vectors and the compositions are useful in clinical, experimental, therapeutic and diagnostic fields, and in the treatment and prevention of cardiac pathologies. [1] is also useful for screening transgenic animals which constitute models for studying certain cardiac molecules for their activity on the regulatory sequences of the gene conding the CARP protein. The present sequence represents the DNA fragment upstream of the coding sequence of a mouse CARP protein.
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TATAGACAAGTGCCTTTAGGGCCCCAGATCCCTTCCCCTCAGGCTGTTTACCCCAGGGAATA
                                                                   1620 AGATATTACTGGGGGGGGTGTGTAGTAGGGGCATCTACATTTTCTTGATA-GGTAGTCATAT
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                                                                                                                 GGATGTCC---TGGGACAAGTTTCCCCTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAA
                                                                                                                                                                                                                1797 AGATATGGCTGTAAGTGTGATGCACAGTGC--TTGCATTTTTCTTGATACGTTAGTCATAT
                                                                                                                                                                                                                                                  GAAAGCTGACAAAGAA--AAAAAGGGCAGTGATGTGGTGCAATGTCAACAGACAGCTGTC
                                                                                                                                                                                                                                                                                                                  CCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1856 CTCCCTCTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2089 GCCACTGGTGGGAGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 13568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI93508 standard; cDNA; 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2
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                      2250 GTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATAG 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1443 AAGGTGGCATGTCATGGGGCCTATTTAGCCCAGACATCACTCCAAAGAATTCCAAACAGA 1502
 GTGTGGAGGGGCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAACATAC 2056
                                                                                                                                                                                                                                                                                                                ankyrin repeat protein; CARP promoter; murine; adenovirus vector; specific; heart disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a human type-5 recombinant adenovirus vector for achieving cardiac-restricted transcription of a gene of interest. The vector comprises inverted terminal repeat (ITR) sequences from human adeno-associated virus (AAV) type 2 (AAA10404-A10405) and a cardiac tissue- specific promoter. In particular, the promoter is that of the cardiomyocyte- restricted cardiac ankyrin repeat protein (CARP) gene. The adenovirus vector is used for targetted gene therapy for heart disease and for evaluating gene function. Cardiac restricted transgene in both neonatal and mature cardiac tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTTATAATGATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1559 CAGTGACACCATAGAGTCCAAGTGCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be achieved to treat inherited and acquired heart diseases. The vector is suitable for tissue-specific use in vivo and in vitro and provides cardiac restricted transcription. The present sequence represents the murine cardiac ankyrin repeat protein (CARP) promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 2247 BP; 609 A; 549 C; 485 G; 589 T; 15 other;
                                                                                                                                                                                                                                                                                 Murine cardiac ankyrin repeat protein (CARP) promoter
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                                                                                                                                                                                 AAA10406 standard; DNA; 2247 BP
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les 567; Conservative
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1998
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P-PSDB;

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Human, congestive heart failure, dilative cardiomyopathy, sudden death, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, rhythm disorder, heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone X83703; CAA58676 protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCCAGCAGGGCCAACTCCAGGGATTCCTTCCACGACAGAAAAACATACAAGACTCCTT
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                                                                                                           Sakurada K;
                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                         DNA sequences, proteins encoded by them and antibodies against useful in diagnosis and treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1901;
                                                                                                           Kawabata A,
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Pred, No. 2.8e-43;
0; Mismatches 5;
                                                                                                         M, Ota T,
Sugano S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                        Claim 20; Page 422-425; 678pp; Japanese
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250..1209
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Nakamura Y,
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                                          (KYOW ) KYOWA HAKKO KOGYO KK
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Best Local Similarity 97.6%;
Matches 242; Conservative
99JP-0280976.
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                                                                                                       H, Yoshisue, Sekine S,
                                                                                                                                                                      WPI; 2001-266308/27
P-PSDB; AAB90787.
                                                              NOJIMA H.
                                                                                                                                                                                                                                                                                    arteriosclerosis
  01-OCT-1999;
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                                                                                                                                                                                                                         the encoded proteins (AAO000010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                The invention relates to human polynucleotides (AAI79941-AAI93841) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1947 TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.1%; Score 229.6; DB 22; Length 1988; 98.0%; Pred. No. 1.2e-43;
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                                                                                                                                                                 Claim 1; SEQ ID NO 13568; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human shear stress-response coding sequence SEQ ID NO: 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 225...,
Pred. No. 1.2e-43;
Trefile 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stress-response protein; vascular disease;
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Matches 145; Conservative
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                                                               2067 CAGCCAAC 2074
                                                                                     242 CAGCCAAC 249
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                                                                                                                                                                             AAS94903;
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                                                                                                                           RESULT 7
AAS94903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methode for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat disease of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial hart disease, congenital heart disease, pericardial disease, valvular heart disease, congenital heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart diseases. The present DNA sequence is expressed sequence tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGTGGGAGTGTTACTTCGG
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Pred. No. 2.8e-43;
0; Mismatches 5; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
                                                                                                                         1391..1401
/*tag= b
/note= "AU-rich mRNA decay element"
                                                                                                                                                                             /*tag= b
/note= "AU-rich mRNA decay element"
                                                                                                   '*tag= b
'note= "AU-rich mRNA decay element'
/product= "Human CAA58676 protein"
198..431
                                                              '*tag= b
'note= "SIMC01-1 cDNA fragment"
 /rag= b //note= "66268 cDNA fragment" | 1604..1753 //note= hote | 1604..1753 //note
                                                                                                                                                                                                                                                                                                                                          Henkel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2a; Fig 10b; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.0%;
Best Local Similarity 97.6%;
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                          Beck J,
                                                                                                                                                                                                                                                                  30-MAY-2001; 2001WO-EP06165.
                                                                                                                                                                                                                                                                                         30-MAY-2000; 2000US-207400P
                                                                                      1302..1306
                                                                                                                                                                1415..1423
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P-PSDB; AAE16633.
                                                                                                                                                                                                                                                                                                                 (MEDI-) MEDIGENE AG
                                                                                                                                                                                                                                                                                                                                          Reuner B,
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122 TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCCAGCTATATAAGCTGACCGGTGTGGAGG

TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG

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                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be useful in the diagnosis of discorders associated with foam cell development such as a therosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the inventially expressed during foam cell differentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2007 GGCCCAGCAGGCCAACTCCAGGGATTCCTTCCACGACAGAAAACATACAAGACTCCTT
                                            182 GGCCCAGCAGCAGCCAACTCCCAGGGATTCCTTCCACGACAAAAACATACAAGACTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1929 GCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA sequence #158 expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 144.4; DB 24; Length 1889; 99.3%; Pred. No. 8.9e-24; tive 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 213; 315pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                    AAS94903 standard; DNA; 1889 BP.
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2049 AAACATACAAGACTCCTTCAGCCAAC 2074
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                                                                                                                                31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a combination of cDNAs (designated BC-CDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-CDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or bind the protein differentially expressed in breast cancer is useful for detecting the expression of a protein in a sample. The BC-CDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast cancer. This sequence represents a differentially expressed breast cancer associated CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=20020156263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     New cDNAs, which are differentially expressed in (metastatic) breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 144.4; DB 25; Length 1889;
Pred. No. 8.9e-24;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer useful for diagnosing or staging, breast cancer, or for monitoring the treatment of breast cancer in an individual
                                                                                                                                                                 Differentially expressed breast cancer associated cDNA #143.
                                                                                                                                                                                        Breast cancer; differential gene expression; BC-cDNA; breast cancer diagnosis; breast cancer monitoring; breast cancer staging; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1889 BP; 613 A; 354 C; 452 G; 469 T; 1 other;
          2049 AAACATACAAGACTCCTTCAGCCAAC 2074
                                125 AAACATACAAGACTCCTTCAGCCAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 182; 30pp; English.
                                                                                           ABX77648 standard; cDNA; 1889 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.38;
                                                                                                                                                                                                                                                                                                               04-OCT-2001; 2001US-0974298
                                                                                                                                                                                                                                                                                                                                      05-OCT-2000; 2000US-238331P
                                                                                                                                          09-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                 US2002156263-A1
                                                                                                                                                                                                                                                                                                                                                              (CHEN/) CHEN H.
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                       24-OCT-2002.
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                                                                                                                   ABX77648;
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                                                                     RESULT 8
ABX77648
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20706 AAGATTAGCATGGCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 20765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF97787 to AAF97829 represent PR primers used in the exemplification of the present invention, and AAF97810 to AAF97812 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer; tumour suppressor; human 1p36 homozygosity deletion domain; tumour; diagnosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAATAAATAAATAAAGAGAAAAGGAAAAAATTAAAAAGAAA 423
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74.1%; Pred. No. 2.4e-12;
tive 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 104-118; 226pp; Japanese.
125 AAACATACAAGACTCCTTCAGCCAAC
                                                                                                                                                                                                                             AAF97854 standard; DNA; 34488 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-2000; 2000WO-JP05930.
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09-MAY-2000; 2000JP-0136266.
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Best Local Similarity
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RESULT 10 AAC66548

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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23092
                                                                                                                                                                                                                                                             17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                 000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                                 000US-0198123
                                 06-NOV-2001 (first entry)
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
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                                                                                                                                                                                                                           09-AUG-2001
   AAK68280;
   47552 AAGATTAGCATGGCCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 47611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47492 AATAACTAAGCACGGTGCTCGCTTCGGCACACATATACTAAAATTGGAACGATACAGAG 47551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIFIA and KIFIB proteins. The sequences disclosed in the invention can be used in the islandiation of similar human proteins and in vector production. In addition, the biallalic markers shown can be used in disease diagnosis and population studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAAATAGGAGCTATACAAAG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGTGAAACATTCCATATATT 377
                                                                                                                                                                                                                     Human, kinesin-like protein, HKLP; KIF1, cell division, cancer,
intracellular transport, neurological disorder, infertility,
biallelic marker, spontaneous abortion, neonatal chromosome disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12 nucleotides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121162 BP; 33272 A; 24108 C; 25842 G; 37919 T; 21 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.7%; Score 97.2; DB 21; Length 121162; Best Local Similarity 74.1%; Pred. No. 3.6e-12; Matches 123; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                                                                                     Human kinesin-like protein HKLP coding sequence contig SEQ ID
AAAAATAAATAAATAAAGAGAAAAGGAAAAAATTAAAAAGAAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dufaure-Gare I, Grel P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 143-175; 199pp; English
                                                                                   AAC66548 standard; DNA; 121162 BP
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AAK68280
ID AAK68280 standard; DNA; 7141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0130217
                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                             WO200063375-A1.
                                                                                                                                                                                                                                                                             aneuploidy; ds
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                                                                                                                                                                                                                                                                                                               Homo sapiens
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PR 14-5EP-2000; 2000US-02334401.

PR 14-5EP-2000; 2000US-02334641.

PR 21-5EP-2000; 2000US-02334623.

PR 21-5EP-2000; 2000US-0233462.

PR 22-5EP-2000; 2000US-0234634.

PR 23-5EP-2000; 2000US-023464.

PR 23-5EP-2000; 2000US-0234186.

PR 23-5EP-2000; 2000US-023418.

PR 23-5EP-2000; 2000US
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM81210 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
cytoteins and polynucleotides may be used in the prevention, diagnosis and
cxample, they may be used to treat disorders associated with decreased
cxpression by rectifying mutations or deletions in a patient's genome
cxpression by rectifying mutations or deletions in a patient's genome
cxpression by rectifying mutations of (1). Additionally, (1)
cytoteins and polynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
cytotein. (1) proteins and polynucleotides may be used to prevent,
c diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
c sequences from the present invention. AAK84942 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3982 CCACCACACCTGGCCGTGAACT-TTTTCTTTCCCTTTATTTTCAAAAAAAATGTTTTCAT 4040
                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3862 ATTTTTTGTATTTTTAGTAGAGGTGTGACACCATGTTGCCCAGGCTAGTTTTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1196 CCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1255 CCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 23092; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.6%; Score 95.6; DB 22; Length 7141; Best Local Similarity 70.3%; Pred. No. 3.3e-12; Matches 156; Conservative 0; Mismatches 64; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7141 BP; 2053 A; 1477 C; 1612 G; 1999 T; 0 other;
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                                                                                                                                                                                                                                    Ruben SM
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AAS28595 standard; DNA; 6040 BP
                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                               08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                      2000US-0251868
2000US-0251869
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2000US-0234998. 2000US-0235884. 2000US-0235834. 2000US-0235836. 2000US-0236367. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0237037. 2000US-0237037. 2000US-0237038. 2000US-0237037. 2000US-0237038. 2000US-0237038. 2000US-0237039. 2000US-0237039. 2000US-0237038.

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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
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anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                                                                                                                   31-JAN-2000; 2000US-0179065.

24-FEB-2000; 2000US-0180628.

24-FEB-2000; 2000US-0180664.

02-MAR-2000; 2000US-0180550.

16-MAR-2000; 2000US-018974.

17-MAR-2000; 2000US-019977.

18-APR-2000; 2000US-0199123.

19-MAY-2000; 2000US-0205515.

07-JUN-2000; 2000US-0205467.

28-JUN-2000; 2000US-0209467.
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                                                                                                          WO200155448-A1
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                                                                 Homo sapiens
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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14-AUG-2000
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01-SEP-2000
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20000S-0241785 20000S-0241786 20000S-0241809 20000S-0241809 20000S-0241809 20000S-0246474 20000S-0246477 20000S-0246477 20000S-0246477 20000S-0246477 20000S-0246476 20000S-0246477 20000S-0246476 20000S-0246528 20000S-0246529 20000S-0246529 20000S-0246529 20000S-0246529 20000S-0246529 20000S-0246610 20000S-0246610 20000S-0246610 20000S-0246610 20000S-0246610 20000S-0246610 20000S-0246610 20000S-0246610 20000S-0246210 20000S-0246210 20000S-0249210 20000S-0249211 20000S-0249211

2000US-0250160. 2000US-0250391. 2000US-0251988. 2000US-0251479. 2000US-0251479. 2000US-0251868. 2000US-0251868.

2000US-0251989. 2000US-0251990. 2000US-0254097.

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2000US-0220964.
2000US-0224518.
2000US-0224519.
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2000US-0218290.
2000US-0220963.
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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28-JUN-2000;
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07-JUL-2000;
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       The present invention relates to the isolation of novel human respiratory antigens (AAU1685-AAU1975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders e.g. vocal cord paralysis, tonsillitis, and laryngitis), ung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel to human respiratory antisens.

Change invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel to human respiratory antisens.

Change invention are useful in gene therapy and antisense therapy.

AAS28161-AAS28764 represent genomic sequences encoding for novel specification, but was obtained in electronic format directly from WIPO.

Cat flp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
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                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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4.6%; Score 95.4; DB 22; Length 6040;
Best Local Similarity 72.8%; Pred. No. 3.5e-12;
Matches 123; Conservative 0; Mismatches 46; Indels 0;
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                                                                                                                                                                                                                                                                                             Disclosure; SED ID No 1029; 546pp; English
                                                                                                   Barash SC, Ruben SM;
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                                                  (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001 (first entry)
                                                                                                                                                 WPI; 2001-476224/51.
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                                                                                                Rosen CA,
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11D AAK88
AC AAK84
XX AC AAK84
XX COT-NC
XX C
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cuplement caids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87650 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                             1022 TTCTGACAAGCTCCCACAGGTGATTCCTTTCCCCACAGCATTTGAGAACTTCAGCTCAAT 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                          3948 TTTTTTTTTAGTTGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAATGCCTGAT 3889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261 CACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATTTTGAA 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3828 CGCCCGGCCCAGTGCCAGTTTCTTTTAGTGTTTTTAGGGAACAACCTAGACAGATTTATCA 3769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4068 TITIGGCTCACTGCAACCTCCGCCTCCTGGGCTTAAGCAATTCTCCTGCTTCAGCTTCCC
                                                                                                                                                                                                                                                                                                                                                                 1082 GACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATATATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                  1142 AGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1202 CT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGCCACTG
                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                           Score 94; DB 22; Length 4181;
Pred. No. 6.6e-12;
1; Mismatches 122; Indels
                                                                                                                                                                                                                                      Seguence 4181 BP; 1137 A; 1031 C; 985 G; 1028 T; 0 other;
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2000US-0180628.
2000US-0184664.
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Best Local Similarity 58.9
Matches 178; Conservative
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 39455; 3071pp + Sequence Listing; English
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                                     17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
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17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
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2000US-0198350.
2000US-0198123.
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2000US-02198146.
2000US-0215135.
2000US-02158515.
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2000US-021585.
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2000US-022528.
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2000US-02258.
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2000US-0231413.
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2000US-0232398
2000US-0232400
2000US-0232401
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2000US-0233064
2000US-0233065
2000US-0234234
2000US-0234234
2000US-023434
2000US-0235844
2000US-0235836
2000US-0235836
2000US-0236367
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2000US-0237039
02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
18-APR-2000; 2
19-MAY-2000; 2
07-JUN-2000; 2
28-JUN-2000; 2
28-JUN-2000; 2
07-JUN-2000; 2
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21 - SEP - 2000
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29 - SEP - 2000
20 - SEP - 200
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11-JUL-2000;
11-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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2000US-0241787 2000US-0241808 2000US-0241809 2000US-0244617 2000US-0246474 2000US-0246474 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246610 2000US-0249211. 2000US-0249212. 2000US-0249213. 2000US-0249214. 2000US-0249215. 2000US-0249215. 2000US-0239935. 2000US-0239937. 2000US-0240960. 2000US-0249264. 2000US-0249265. 2000US-0249297. 2000US-0249299. 2000US-0249300. 2000US-0250160. 2000US-0250391. 2000US-0241221. 2000US-0241785. 2000US-0241786. 2000US-0251988. 2000US-0256719. 2000US-0251479. 000US-0249218 000US-0249244 2000US-0251868 2000US-0251869 000US-0249245 2000US-0251030 2000US-0251856 13-OCT-2000; 13-OCT-2000; 20-OCT-2000; 20-OC 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 7-NOV-2000; 7-NOV-2000; 7-NOV-2000; 7-NOV-2000; 

(HUMA-) HUMAN GENOME SCI INC

Ruben Barash SC, WPI; 2001-483426/52 Rosen CA,

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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

+ Sequence Listing; English NO 23094; 3071pp Disclosure; SEQ ID

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2000US-0220964.
2000US-0224518.
2000US-0224519.
                                                                                                                            2000US-0225213.
2000US-0225214.
2000US-0225266.
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2000US-0229287.
2000US-0229343.
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2000US-0230438.
2000US-0231242.
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2000US-0218290.
2000US-0220963.
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2000US-0225758.
2000US-0225759.
2000US-0226279.
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000US-0231244
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       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cutivity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polymucleotides may be used to product on of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54920 and AAK64703 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                  1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
                                                                                                                                                                                                                                                                                                                                                                                      CCTAAGCT-AAGCAATCTTCCTGTCTCTCCCCCCAAAATGTTGGGATTACAGGTGTAAG 1254
                                                                                                                                                                                                                                                                                                                                                                                                             3922 CCTGAGCTCAGGCAATCTGCCTACCTCGGCCTCCCAAAATGCTAGGATTACAGGTGTGAG 3981
                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCAT 1314
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                                                                                                                                                                                                                                                                                                                                                           3862 ATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGCCCAGGCTAGTTTTGAACT
                                                                                                                                                                                                                                                                                                       Gaps
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69.8%; Pred. No. 7.9e-12;
tive 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                   Sequence 7141 BP; 2053 A; 1476 C; 1615 G; 1997 T; 0 other;
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AAK71437 standard; DNA; 52845 BP.
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16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0190076.

18-APR-2000; 2000US-0190131.3.

19-MAY-2000; 2000US-0205515.

07-JUN-2000; 2000US-0209467.

28-JUN-2000; 2000US-0209467.

30-JUN-2000; 2000US-0215135.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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Best Local Similarity 69.8
Matches 155; Conservative
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                         2000US-0246474
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2000US-0246526
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20-OCT-2000;
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1195 TCCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAAG

51170 TAATTTTTGTATTTTTGGTAAAGATGGGGTTTCACCATTTTGGCCAGGCTGGTCTTGAAT 51111

1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCAGGCCTAGTATTGAAC 1194

polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169

supplement the patients own production of (I). Additionally, (I)

represent sequences used in the exemplification of the present invention.

Sequence 52845 BP; 14698 A; 11081 C; 10505 G; 16561 T; 0 other

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0; Gaps

Score 93.6; DB 22; Length 52845; Pred. No. 1.9e-11; 0; Mismatches 64; Indels 0;

Query Match
Best Local Similarity 67.3%;
Matches 132; Conservative

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51050 TCACTACACCCAGCCTTTAGATTTGTGTAAGTACATTCTATGAGGTTCACACAATGATGA 50991

1255 CCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCAT 1314

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Search completed: November 17, 2003, 23:52:55
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Query Match
Best Local Similarity 73.3
Matches 118; Conservative
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ORGANISM: Human
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Compugen Ltd
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S-09-641-638-199
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US-09-114-638-651

US-09-641-638-651

US-09-641-638-651

US-09-78-995-3

US-09-729-995-3

US-09-102-995-3

US-09-984-890-3

US-09-984-890-3

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       GenCore (c) 1993
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Sequence 3, Application US/09740041

Patent No. 6562593

GENERAL INFORMATION:
APPLICANT: MERKULOV, KAR1 et al
TITLE OF INVENTION: ISCLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01001
CURRENT APPLICATION NUMBER: US/09/740,041
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 66804
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Sequence 5, Application US/09212971B

Sequence 5, Application US/09212971B

Sequence 5, Application US/09212971B

SERVERAL INFORMATION:

APPLICANT: MacKenzie, Alexander E

APPLICANT: Liston, Peter r

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine APPLICANT: Pratt, Christine APPLICANT: Trang, Service Christine APPLICANT: Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Trang, Tr
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                                                               US-10-060-332-3
US-09-345-806-3
US-09-345-808-3
US-09-873-404-3
US-07-695-4728-4
US-09-106-375-4
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APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Daird, Stephen
APPLICANT: Tsang, Berjamin K
APPLICANT: Tsang, Benjamin K
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APPLICANT: Trang, Benjamin K
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APPLICANT: Trang, Benjamin K
APPLICANTON: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DISEASE
FILE REPERENCE: 07891/00903
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT PILING DATE: 1997-02-13
FRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH 6669
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4.3%; Score 89.4; DB 4; Length 6669;
Best Local Similarity 73.1%; Pred. No. 7.2e-13;
Matches 128; Conservative 0; Mismatches 46; Indels 1
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FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
TELEFAX: 617-428-7045
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NAME/KEY: variation
LOCATION: (3677)...(3951)
OTHER INFORMATION: n can be any nucleotide
US-09-617-053A-5
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                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexand
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Sequence 5, Application US/08800929A

Sequence 5, Application US/08800929A

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: MacKenzie, Alexander E

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

TITLE OF INVENTION: IDPECTION AND MODULATION OF

TITLE OF INVENTION: DETECTION

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1290 TCCTGACCTCAAGTGATCCACTTGTCTTGGCCTCCCAAAATGCTGGGATTACAGGCGTGA 1349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.3%; Score 89.4; DB 3; Length 6669;
Best Local Similarity 73.1%; Pred. No. 7.2e-13;
Matches 128; Conservative 0; Mismatches 46; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110
COMPUTER REDBLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
                   TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: variation
CCATION: (3677)...(3951)
COTHER INFORMATION: n can be any nucleotide
VS-09-212-911-5
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176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
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US-08-800-929A-5
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us-10-005-337a-2.rni

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RESULT 7

US-09-978-197-3

US-09-978-197-3

Sequence 3; Application US/09978197

Fatent No. 6403353

GENERAL INFORMATION:

APPLICANT: VAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01178DIV

CURRENT FILING DATE: 2001-10-17

PRIOR APPLICATION NUMBER: 09/813,817

PRIOR FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ 10 NO 3

LENGTH: 59065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09641638

Patent No. 6432648

GENERAL INFORMATION:
APPLICANT: Buumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFRENCE: GENGET.051CP1
CURRENT APPLICATION NUMBER: US 09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR PRILOK PAPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
                                                                                                 11864 TCCTGACCTCAAGTGATCCACCTGCCTCCGCTCCCAAAGTGCTGGGATTACAGGTGTGA 11923
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                           1; Gaps
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                           Indels
                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.2%; Score 87.8; DB 4;
Best Local Similarity 78.1%; Pred. No. 4.2e-12;
Matches 118; Conservative 0; Mismatches 32;
  78.1%; Pred. No. 4.2e-12;
tive 0; Mismatches 32
                                                                                                                                                                                                                                                                                                                 11924 GCCACTGCACCTGGCTGGAAGGAGTGATCTT 11954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11924 GCCACTGCACCTGGCAGGAGGAGTGATCTT 11954
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  Best Local Similarity 78.1
Matches 118; Conservative
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ORGANISM: Human
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US-09-641-638-36
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Patent No. 6340583

GREEAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THREOF
FILE REPERENCE: CLOO1178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 59065
                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09984890

Sequence 3, Application US/09984890

Patent No. 6492156

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1306
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                        1290 TCCTGACTCTAAGTGATCCACTTGTCTTGGCCTCCCAAATGCTGGGATTACAGGCGTGA 1349
1230 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATTTTGGCCAGGCTGGTTTTGAAC 1289
                                             1195 TCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAA 1253
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                                                                                                                                                                     1350 GCCACTGCACCAGGCAGAGGCCTCTTTTTATCTCTTTTTGGCCTCTACAGG 1404
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 72.1
Matches 129; Conservative
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; ORGANISM: Human
US-09-813-817-3
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LENGTH: 75395
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US-09-984-890-3
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NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62
NAME/KEY: allele
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OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 12854..13023
DIHER INFORMATION: exon 10
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LOCATION: 16775..16945
OTHER INFORMATION: exon 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 17063..17554
OTHER INFORMATION: exon 14
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LOCATION: 12254..12340
OTHER INFORMATION: exon 9
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
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LOCATION: 5996..6099
OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
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OTHER INFORMATION: exon 8
                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3124.3297
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 7379..7522
OTHER INFORMATION: exon 7
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LOCATION: 5552..5633
OTHER INFORMATION: exon
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                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1123_.3123
                                                                                            ORGANISM: Homo sapiens
                 20674
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Sequence 651, Application US/09641638

Patent No. 6432648

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Cohem., Annick
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REPRENCE: GENEST: 051.CP1
CURRENT APPLICANT: 000-08-16

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REPRENCE: GENEST: 051.CP1

CURRENT APPLICATION NUMBER: US 09/641,638

CURRENT FILING DATE: 2000-08-16

PRIOR PILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

SOFTWARE: Patent.pm

SEQ ID NO 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COTHER INFORMATION: 10-349-47.mis1, potential
NAME/KEY: misc_binding
LOCATION: 479.498
LOCATION: 10-349-47.mis2, potential complement
NAME/KEY: primer bind
LOCATION: 432.451
COTHER INFORMATION: upstream amplification primer
NAME/KEY: primer bind
LOCATION: 829.848
COTHER INFORMATION: downstream amplification primer
NAME/KEY: misc binding
LOCATION: 466.490
LOCATION: 466.490
LOCATION: 466.490
LOCATION: 466.490
LOCATION: 466.490
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4.2%; Score 86.8; DB 4; Length 956;
Best Local Similarity 76.6%; Pred. No. 1.5e-12;
Matches 118; Conservative 1; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
LOCATION: 478
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: misc binding
LOCATION: 458..477
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| PRIOR APPLICATION NUMBER: US 09/275,267 | PRIOR FILING DATE: 1999-03-23 | PRIOR FILING DATE: 1999-03-21 | PRIOR PILING DATE: 1999-02-12 | NUMBER OF SEQ ID NOS: 1304 | SOFTWARE: Patent.pm | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 36 | SEQ ID NO 
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapiens
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NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTA or TITITT
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OTHER INFORMATION: 10-511-337 : insertion of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : deletion of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymory
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymory
NAME/KEY: allele
LOCATION: 1599
OTHER INFORMATION: 10-509-284 : polymory
NAME/KEY: allele
LOCATION: 159
OTHER INFORMATION: 10-509-284 : polymory
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion
OTHER INFORMATION: 5'regulatory region
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: polymorphic base A or G
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OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
                                                                                                                                                                                           : polymorphic base C or
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                   : polymorphic base G or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 6141
OTHER INFORMATION: 10-346-263 :
MAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 :
NAME/KEY: allele
                                                                                                                                                                                                                          LOCATION: 2934
OTHER INFORMATION: 10-513-352
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365
NAME/KEY: allele
LOCATION: 3802
                                                                                                            LOCATION: 2832
OTHER INFORMATION: 10-513-250
                                                                                                                                                                       LOCATION: 2844
OTHER INFORMATION: 10-513-262
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 4062
OTHER INFORMATION: 10-343-231
NAME/KEY: allele
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OTHER INFORMATION: 10-343-278
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 4170

JOTHER INFORMATION: 10-343-339

ARME/KEY: allele
LOCATION: 5903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 10-347-111
NAME/KEY: allele
LOCATION: 6429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: 6484
OTHER INFORMATION: 10-347-220
NAME/KEY: allele
                                                         LOCATION: 2623
OTHER INFORMATION: 10-512-318
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION: 4088

NTHER INFORMATION: 12-206-366

NAME/KEY: allele
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OTHER INFORMATION: 10-347-271
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 10-347-348
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391
LOCATION: 2341
OTHER INFORMATION: 10-512-36
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION: 10-346-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION: 6467
THER INFORMATION: 10-347-203
AME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                              NTHER INFORMATION: 12-206-81
NAME/KEY: allele
LOCATION: 4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: 10-347-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 10-346-23 AME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: 6338
THER INFORMATION: 10-347-74
                                                                                                                                                     NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 8608
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OCATION: 6375
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8198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1116 GTCTCATTTTTBTCATATATATATATATATTTGTGGTAGAGATGGGATTTTGCCATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8139 GCCACCATGTGGGCCTGGCTAATTTTTGTATTTTTTTTTGTAGATGGGGTTTCGCCATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.2%; Score 86.8; DB 4; Length 20674;
Best Local Similarity 76.6%; Pred. No. Se-12;
Matches 118; Conservative 1; Mismatches 34; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
ITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                                                                    : polymorphic base G or C
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                                                                                                                                                                                                      : polymorphic base G or T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : polymorphic base C or
OTHER INFORMATION: 10-349-97 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                             : polymorphic base C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.2%; Score 86.2; DB 4; Best Local Similarity 75.5%; Pred. No. 1.3e-11; Matches 120; Conservative 0; Mismatches 38;
                                                                                                                                      : deletion of CTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 12171
LOCATION: 12171
LOCATION: 12171
NAME/KEY: allele
LOCATION: 12429
COTHER INFORMATION: 10-350-332:
NAME/KEY: allele
LOCATION: 13341
COTHER INFORMATION: 10-507-170:
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-321:
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-331:
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-331:
NAME/KEY: allele
                                                                                                                               OTHER INFORMATION: 10-349-216 : NAME/KEY: 311ele : LOCATION: 8775 OTHER INFORMATION: 10-349-224 : NAME/KEY: 311ele : LOCATION: 8926 OTHER INFORMATION: 10-349-368 :
                NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                       NAME/KEY: allele
LOCATION: 8777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 13535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-798-096-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
US-09-798-096-10
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Sequence 7, Application US/09657474
Patent No. 6399762
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LOCATION: all n positions
OTHER INFORMATION: n=a, c, g, or
  ; ORGANISM: HOmo sapiens
; ORGANISM: HOmo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, o)
US-09-268-992-7
                                                                                                                                                                                  4.1%;
                                                                                                                                                                              Query Match
Best Local Similarity 72.59
Matches 111; Conservative
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Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-09-657-474-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16818 TCCTAACTCAGGTGATCTGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAG 16759
                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09729995

Patent No. 6426206

GENERAL INFORMATION:
APPLICANT: WEL, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT APPLICATION NOWELS: 2000-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1195 TCCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1135 TATATATATATTGTGGTAGAGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAAC
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US-09-268-992-7/c
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
    APPLICAMY: Chen, H.
    APPLICAMY: Chen, H.
    APPLICAMY: Chen, H.
    APPLICAMY: Preimer, N.
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
    ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
    TITLE OF INVENTION: NUMBER: US/09/268,992
    CURRENT FILING DATE: 1999-03-16
    EARLIER PILING DATE: 1999-01-22
    EARLIER FILING DATE: 1999-01-22
    EARLIER FILING DATE: 1998-06-05
    EARLIER FILING DATE: 1998-06-05
    EARLIER FILING DATE: 1998-06-05
    EARLIER FILING DATE: 1998-03-16
    NUMBER OF SEQ ID NOS: 84
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 7
    LENGTH: 72604
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al Similarity 77.6%; Pred. No. 9.2e-12;
104; Conservative 0; Mismatches 30.
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16758 CCACCGCACCCGGC 16745
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Best Local Similarity
Matches 104; Conserv
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 29629
                                                                                                                                                                                                                                                                      RESULT 11
US-09-729-995-3/c
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57521
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      Length 72604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Freiner, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORD;
FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: 09/268,992
PRIOR APPLICATION NUMBER: 09/268,992
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR PAPLICATION NUMBER: 60/106,056
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 60/078,044
PRIOR FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH 1200
Score 85.8; DB 4; Length 7
Pred. No. 1.5e-11;
0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                              57460 CCACCACACCCGGCTGTATGAAGCATGTTTTTA 57428
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                                                                                                                                                    GENERAL INC. 6472130

GENERAL INCOMMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01306
CURRENT PAPLICATION NUMBER: US/09/984,890
CURRENT PAPLICATION NUMBER: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 75395
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Patent No. 6492153
GENERAL INFORMATION:
GAUGERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THERED MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERED PROTEINS, AND USES
TITLE OF INVENTION: THERED PROTEINS, AND USES
TITLE OF INVENTION: THERED PROTEINS, AND USES
TITLE OF INVENTION: THERED PROTEINS, AND USES
TITLE OF INVENTION: THERED PROTEINS, AND USES
TITLE REFERENCE: CLOO1043
CURRENT APPLICATION DAMBER: US/09/759,359A
CURRENT PILLING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
LENGTH: 90541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 75395;
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57460 CCACCACACCCGGCTGTATGAAGCATGTTTTA 57428
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1; Mismatches
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                                                                   RESULT 14
US-09-984-890-3/C
; Sequence 3, Application US/09984890
; Patent No. 6492156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION; (1)...(75395)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 76.0°
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 78.6
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Human
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US-09-759-359A-3/c
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November 17, 2003, 23:33:10 ; Search time 992.544 Seconds (without alignments) 6829.176 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appliance 180, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 182, Appliance 182, Appliance 182, Appliance 183, Appliance 183, Appliance 184, Appliance 184, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance 185, Appliance Sequence 2, Appli Sequence 1, Appli Description SUMMARIES 14 111 112 113 113 Query Match Length DB 300000 119040 32220 Score Result Š

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Gaps

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0; Indels

Query Match
99.9%; Score 2071.6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2074; Conservative 0; Mismatches

TYPE: DNA ORGANISM: Homo sapiens

US-10-005-337A-2

DB 14; Length 2074;

120

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1 CTGCAGCAAGTTACTTAATGTTTTTTGCCTCAGCATCCTCTCTGTAAAATGAGAGCATTA 1 CIGCAGCAAGTIACTIAATGTTTTTTGCCTCAGCATCCTCTCTGTAAAATGAGAGCATTA

180

61 GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAAA 120

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	ublica	tion No	5. US2	Publication No. US20030039984A1	984A1	١ .	
	ENERAL	GENERAL INFORMATION:	MATION				
	APPLIC	ANT: BE	ENOIT,	BENOIT, Patrick	u		
	APPLIC		SCHWAR	SCHWARTZ, Bertrand	ranc	77	
••	APPLIC		SRANEL!	LEC, Die	lier		
•••	APPLICANT:		CHIEN,	Kennet	я		
	TITLE	OF INVE	NOILNE	: SEOUE	CES	UPSTREAM OF THE CARP GENE.	VECTORS CONTAINING
	TITLE	OF INVE	NOILNE	OF INVENTION: THEM AND	AND	USES THEREOF	
	FILER	EFERENC	E: 03	FILE REFERENCE: 03806.0530-0000	00-0	000	
	CURREN	IT APPLI	CATIO	N NUMBER	. us	CURRENT APPLICATION NUMBER: US/10/005.337A	
	CURREN	IT FILIN	VG DAT	E: 200	1-12	-0.7	
. ••	PRIOR	PRIOR APPLICATION NUMBER	ATION 1	NUMBER:	ns	60/251,582	
	PRIOR	FILING DATE	DATE:	$\overline{}$	2-07		
	NUMBER	Q.	H	08:5			
•-	SOFTWARE	RE: Pat	entIn	Ver. 2	ન.		
٠.	SEQ ID NO						
••	LENGTH:	H: 2074					
	TYPE:	ANG					

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US-10-240-965-158
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                                                                                                                                                                                                                                                                                                                1598 TTAGAACACGGTCAGCTGTGCACTAATTATGGCCAGTGACACATAAGAGTCAAAGT 1657
                                                                                                                                                                                                                                                                                                                                                                                      1658 GCATTACTGAATGCTTTCAATTCTCCCTAATGCTGGTACGATGCCATGTCACAGGCCCAT 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGATCCCTTCCCCTCAGGCTGTTTACCCCAGGGAATAGGATGTCC---TGGGACAAGTT 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccarcrccrrcccrcggcrgariarcccagaaaiaggargrcccaaagcaacacrrc 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1582 TCCCCTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAAGATATTACTGGGGGTGTGATA 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1642 TGTAGGGCATCTACATTTTCTTGATA-GGTAGTCATATGAAAGCTGACAAAGAA--AAAA 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGACTIGCATIGCTGAGCGATGTGATCACCACAAAGGAATGGCCCTCTCACATTTCTT 1817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCTTCTAGCTTCCCAGAC 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2131 ACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCAGGGGTG 2190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998 GTGTGGAGGGCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAACATAC 2056
                                                                                                                                                                                                                                                         1540 rererererescarcaerresceceerringsser--agarcereratascerreagar
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                                                                                                                                                                                                                                                                                             TTAGAACACGGTAAGCATGTCATGTGCTA---ATGGCCAGTGACATCATAAAAGAAAGT
                                                                                                                                                                                                                                                                                                                                                                   GCATTACTGAATGCTTTCAATGTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTA
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                                                                                                                                                                                                                     1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     22;
                                                                                                                                                 DB 14; Length 2358;
                                                                                                                                               Score 367.8; DB 14; Length
Pred. No. 1.2e-83;
0; Mismatches 162; Indels
                                                                                                                                               17.78;
                                                                                                                                              Query Match
Best Local Similarity 76.4
Matches 597; Conservative
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 2358
                                                                    TYPE: DNA
CORGANISM: Mus musculus
US-10-005-337A-1
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RESULT 3 US-09-974-298-182 Sequence 182, Application US/09974298 ; Parent No. US20020156263A1

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US-09-923-876-5218
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                                                                                                                                                            5 GAGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA 64
                                                                                                                      5 GAGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA 64
                                            Gaps
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0
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  Score 144.4; DB 12; Length 1889;
Pred. No. 2.6e-26;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/10252157
Publication No. US20030190640A1
GENERAL INFORMATION:
APPLICANT: FARTSON, Cechia I.
TILLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER;
FILE REFERENCE: PA-0027-1 US
CURRENT APPLICATION NUMBER: US/10/252,157
CURRENT APPLICATION NUMBER: 602-10-01
PRIOR APPLICATION NUMBER: 602-10-01
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030190640A1 332919.4
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APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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LOCATION: 1655-1681, 1882
OTHER INFORMATION: a, t, c, g, or other
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    7.0%;
Query Match
Best Local Similarity 99.33
Matches 145, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 145; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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US-10-084-817-217
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Sequence 5218, Application US/09923876

Sequence 5218, Application US/09923876

Patent No. US20020013958A1

GENERAL INPORMATION:
APPLICANT: Lalqudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Ranigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT PILING DATE: 2001-08-06
PRIOR PILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332

NUMBER OF SEQ ID NOS: 6332

SEQ ID NO 5218
LENTH: 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.8%; Score 141.4; DB 14; Length 1325; Best Local Similarity 99.3%; Pred. No. 1.3e-25; Matches 142; Conservative 0; Mismatches 1; Indels 0;
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                             CURRENT FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 217
LENGTH: 1325
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030119009A1 183198CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | FEATURE: | NAME/KEX: misc feature | NAME/KEX: misc feature | NAME/KEX: misc feature | NAME/KEX: unsure | LOCATION: 100, 122, 129 | LOCATION: 110:00MATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | LOCATION: a, t, c, g, or other | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218 | US-09-923-876-5218
CURRENT APPLICATION NUMBER: US/10/084,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: 1258
STOPER INPORMATION: a, t, c, g, or other
US-10-084-817-217
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PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/225,757

PRIOR APPLICATION NUMBER: 60/226,868

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2000-06-16

PRIOR PILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/225,267

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-08-14

PRIOR FILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-09-14

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: 60/234,223

PRIOR APPLICATION NUMBER: 60/234,234

PRIOR PILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: 60/234,234

PRIOR APPLICATION NUMBER: 60/234,234

PRIOR PILING DATE: 2000-09-30

PRIOR PILING DATE: 2000-08-19

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PRIOR PILING DATE: 2000-08-19
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PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/240,299
PRIOR APPLICATION NUMBER: 60/241,785
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR PILING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 2000-12-08
PRIOR PILING DATE: 2000-09-29
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                                          61 AAGCTGNACCGGTNTGGAGGGGCCCAGCAGGCCAACNCCAGGGANTCCTTCCACGACAG 120
                                                                                                                                                                                                                                                                                                                                                  Sequence 1029, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICATT ROSEN et al.
; TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1029
; SEQ ID NO 1029
; LENGTH: 6040
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TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008C1

CURRENT APPLICATION NUMBER: US/10/074,095

CURRENT FILING DATE: 2002-02-14

PRIOR PEDICATION NUMBER: 09/764,860

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-8

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-11

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR PILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-16

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-07-11
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                                                                                                                                2047 AAAAACATACAAGACTCCTTCAGCCAAC 2074
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Publication No. US20030077704A1
GENERAL INFORMATION:
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Best Local Similarity 72.8
Matches 123; Conservative
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; ORGANISM: Homo sapiens
US-09-764-860-1029
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PRIOR PELICATION DATE: 2000-0929

PRIOR FILING DATE: 2000-10-02

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PRIOR FILING DATE: 2000-10-03

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PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-13

PRIOR PELICATION NUMBER: 60/240,960

PRIOR FILING DATE: 2000-10-13

PRIOR PELICATION NUMBER: 60/246,474

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PRIOR PELICATION NUMBER: 60/226,139

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NAME/KEY: misc feature
LOCATION: (1)...(300000)
COTHER INFORMATION: where n may be a or g or c or t/u, unknown or other US-10-262-552-33
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Publication No. US20030125289A1
GENERAL INFORMATION:
APPLICANT: Gelb, Bruce D.
TITLE OF INVENTION: NOONAN SYNDROME
FILE REFERENCE: 2420/1J859-US1
CURRENT APPLICATION NUMBER: US/10/262,552
CURRENT FILING DATE: 2002-10-01
PRIOR PELING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3:1
SEQ ID NO 33
LENGTH: 300000
                           FRIOR APPLICATION NUMBER: 60/231, 414

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

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PRIOR PLING DATE: 2000-09-14

PRIOR PLING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 60/233, 064

PRIOR PLING DATE: 2000-09-14

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PRIOR APPLICATION NUMBER: 60/232, 399

PRIOR PLING DATE: 2000-09-14

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ORGANISM: Homo sapiens
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Length 300000

4.6%; Score 94.8; DB 14; 77.1%; Pred. No. 3.3e-12;

Query Match Best Local Similarity

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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT' Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
FRIOR PLING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
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FRIOR FILING DATE: 1990-09-28
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                                                                                                                                                                                                                                                                                                                                                              Query Match
4.5%; Score 93.2; DB 10;
Best Local Similarity 79.2%; Pred. No. 2.2e-12;
Matches 122; Conservative 1; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30413 TTAGGATTATAGGGGGGGCACCACCTGGCT 30446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1236 TTGGGATTACAGGTGTAAGCCACTGCACCCGGCT 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.5%; Score 92.6; Di
Best Local Similarity 73.0%; Pred. No. 2.6e
Matches 119; Conservative 0; Mismatches
                                    LENGTH: 32220

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9867)
US-09-764-877-3933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Human
US-10-027-632-95562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-027-632-95562
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       SEQ ID NO 3933
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                                                                                                                                                                                                                                                       35135 GTGCCCAGCCTACATACCTTGGTCTTGACCCTTTTTCCATATTTTATTTTATTTTATTTTT 85076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85195 GCTCAAACAATCCTCCTCCTTCAGCCTCCCAAAGTGCTGGGATTGCAGGTGTGAGCCACT 85136
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                                                                  1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAAC
                                                                                                                                                                                                          1195 TCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAA
       1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         131020 GCCACCGCAGCCGACAAACTTTGTTTTTTTTCCTCTTTTTTGTTG 131065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09911077A
Publication No. US20030114399A1
Publication No. US20030114399A1
Publicant BLAKELY, RANDY D.
APPLICANT: APPRASUNDARAM, SUBRAMANIAM
APPLICANT: FERGUSON, SHAWN
TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER CDNA
FILE REFERENCE: VBLT:008US
CURRENT APPLICATION NUMBER: US/09/911,077A
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE PALENTIN VEY: 2.1
SEQ ID NO 19
LENGTH: 119040
                                                                                                                                                                                                                                                                                                                                                       1254 GCCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTG 1299
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Sequence 3933, Application US/09764877
Fatent No. US20020147140A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOS
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
   37; Indels
0; Mismatches
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LOCATION: (2347)..(90873)
COTHEN INFORMATION: N = A, C, G or T/U
US-09-911-077A-19
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Matches 128; Conservative
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ORGANISM: Homo sapiens
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US-09-911-077A-19/c
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,318
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PRIOR FILING DATE: 2000-04-20
PRIOR PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
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440 TCACTGCATCTGGCCAAAATTTTCTTTTTTTTTTTTTT 482
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                    ; Sequence 95563, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 73.0
Matches 119; Conservative
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US-10-027-632-95562
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US-10-027-632-95563
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4.5%; Score 92.6; DB 13;
Best Local Similarity 73.0%; Pred. No. 2.6e-13;
Matches 119; Conservative 0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 18, 2003, 07:42:07 Job time : 998.544 secs
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 95562
                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-95562
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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BF738217 CM3-KT003
BF829139 MR1-HN007
AZ335882 1100-G5G12
BF415552 U1-R-CA1-
BZ260574 CH230-285
AZ406305 1M0175C06
AA947380 cd86604 S
BF724783 bx08f06 y
BF420140 U1-R-CA1-
AQ187593 HS_132 A
B1438856 icZ7e07. x
B1438856 icZ7e07. y
BG390793 602416521-AQ468422 nc78f02. r
AQ19862 CIT-HSP-2
AQ48422 nc78f02. r
AQ343576 RPC111-12
AQ219900 HS_3252 A
AZ355944 1MG112419
AF289601 HOMO sapi
AN720761 AV720761
AV720761 AV720761
AV7207651 AV720761
AV72076514 AV720761
AV720765 AV720761
AV720765 AV720761
BE791763 GG221956
BF791763 GG221956
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AQ895064 HS 3175 A
CD520493 AGENCOURT
A1288531 q191a04.x
                          AQ207760 HS 3026 B
AA494075 ng61c08.5
AA917468 ol51f11.8
BC038619 Homo sapi
AI039619 ox28f05.x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ480395 10-236B22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-236B22
           AQ584530 RPCI-11-4
CD244827 AGENCOURT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other GSSs: RPCI-11-236B22.TJ
Other GSSs: RPCI-11-236B22.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 522)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
BY07997
AC5848530
CD2448530
AA494075
AA494075
AA917468
BC038619
BC139619
BF139619
AZ35882
BF829139
AZ35882
BF415552
BF415552
AA947380
                                                                                                                                               BF724783
BF400140
AQ187856
B1439182
B64390793
AQ108862
AA468422
AA468422
AA468422
AA468422
AA365944
AF28601
AF28601
AR848825
AA848825
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AA720761
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AQ109988
BF791763
BM472183
T39841
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 Homo sapiens (human)
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AZ295534 RPCI-23-1
AU139209 AU139209
BY091041 BY091041
                                                                November 17, 2003, 23:31:10 ; Search time 4326.29 Seconds (without alignments) 11651.427 Million cell updates/sec
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                                                                                                                              1 ctgcagcaagttacttaatg......acaagactccttcagccaac 2074
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         5.1.6
Compugen Ltd.
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                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
         version :
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Maximum Match 100%
Listing first 45 summaries
                                               nucleic search, using sw model
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AZ295534
AU139209
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Gapop 10.0 , Gapext 1.0
         GenCore (c) 1993
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em_esthum:.*
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12.6
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8.7
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461.2 260.6 241 181

Score

Result Š.

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-105P3"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                    Mammalia; Eutheria;
1 (bases 1 to 586)
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Mus musculus genomic clone RPCI-23-105P3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403
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library availability, please contact Pieter de Jong pleterAdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.Seq primer: T7 class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                       /cell type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGCCACTGCACCGGC
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Pred. No. 2.5e-19;
1; Mismatches 5; Indels
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                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="GDB:7590285"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                 /clone="RPCI-11-236B22"
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1. .522
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Mus musculus (house mouse)
Mus musculus
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RPCI-23-105P3.TJ RPCI-23 genomic survey sequence.
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Best Local Similarity 97.7%;
Matches 510; Conservative
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/sex="Femaic"
/lab.host="DH108"
/lab.host="DH108"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Pemale C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination OF EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetant cells (BRL Life Technologies). "
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B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhaogeigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Feiter de Jone
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 105 row: P column: 3
Seq primer: SP6
Class: BAC ends.
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Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Other GSSs: RPCT-23-105P3.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Pax: 301 838 0200
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12.6%; Score 260.6; DB 21
Best Local Similarity 75.9%; Pred. No. 1.8e-07;
Matches 403; Conservative 0; Mismatches 114
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Mus musculus (house mouse)
Mus musculus
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 TICCCAGGITGGAAGATTAICICACCCGGCCCCAGCTAIATAAGCTGACCGGTGTGGAGG 2006
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-438-52-3986
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
Fax: Bran cDNA project; 57. 23'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                   434 Trcccasscrissasarrarcrcaccascccrascrararaa-cosscristrates
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Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 241; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/tissue_type="placenta"
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/note="Vector: pME185FL3"
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Eukaryota, Musaculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

CE 1 (bases 1:to 371)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Salto,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
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Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
M., M., Shanai,A., Kawaji,H., Kawasawa,Y., Lenhard,B., Lyons
N., Maglott,D.R., Maltais,L., Marchioni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Odido,T., Pavan,W.J., Percea,G.,
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N., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Tasadale,C., Walls,C., Walming,L.G., Wahlestedt,C., Wang,Y.,
Watanabe,Y., Wells,C., Wilming,L.G., Wanisaw-Boris,A., Yanagisawa,M., Sato,K., Shiraki,T., Wahlestedt,C., Wang,Y.,
Watanabe,Y., Walls,C., Wilming,L.G., Wanno,H., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Waki,K., Sasaki,D., Arakawa,T., Futuda,S., Harozane-Kishikawa,T., Konno,H., Nakawa,R., Arakawa,T., Futuda,S., Haraka,A., Hashizume,W., Imotani,K., Ishiaa,R., Arakawa,T., Futuda,S., Haraka,A., Yashiaia,A., Yashiaia,A., Yashaya,T., Marayashiao,A., Yashiaia,A., Yashayashiao,A., Yashiaia,A., Yashiaia,A., Yashaya,T., Marayashiao,A., Yashiaia,A., Yashiaia,A., Yashiagashia,A., Yashiaia,A., Yashiaia,A., Yashiaia,A., Yashayashizaki,Y., Waterseton,R., Inch,M., Kagawa,T., Maraka,A., Yashiio,M., Waterseton,R., Inch,M., Kagawa,T., Maraka,A., Yashiiaa,A., Yashiiaa,A., Yashiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yanghiiaa,A., Yang
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BY091041 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630084E21 5', mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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BY079997 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630022E19 5', mRNA sequence.
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Nokazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,M., Salto,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Bradt,D., Brusic,V., Chothia,C., Corbani, L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 GCTGGTGGAGGGCTCCACAGGGCCCAGTTCCAGGGGTTCATCCACAAGAGAAAAAAC 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="heart"
/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Computer-based methods for the mouse full-length cDNA
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/strain="C57BL/6J"
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Normalization and subtraction of cap-trapper selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length
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Score 158.4; DB 13; Length 353; Pred. No. 0.27;

7.6%;

Query Match Best Local Similarity

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1155

1214 265

205

145

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/organism="Homo sapiens"

/mol_type="mknA"

/db_xref="taxon:9606"

/clone="INAGE:30376302"

/tissue_type="White Matter"

/dev_stage="Unknown"

/lab_host="Dhi0B-TON A (T1 and T5 phage resistances)"

/clone lib="NIH MGC 181"

/clone lib="NIH MGC 181"

/note="Vector: pGNV-SPORT6.1; Site_1: NotI; Site_2: ECORV

/note="Vector: pGNV-SPORT6.1; Site_1: NotI; Site_2: CORV

/note="Vector: pGNV-SPORT6.1; site_1: NotI; Site_2: ECORV

/note="14" A library is oligo-dT primed and directionally

cloned (ECORV site is destroyed upon cloning). Average

insert size 1.42 kb. Library was constructed by

insert size 1.42 kb. Library was constructed by

insert size 1.42 kb. Library was constructed by

invitrogen). Note: this is a NIH MGC Library."
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I (Dases 1 to 827)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
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Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: NDAM438 row: 1 column: 07
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AGENCOURT 14096429 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30376302 5', mRNA sequence.
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                                                                          Length 343;
                                                                                                                                    Indels
                                                                      Score 98.6; DB 28;
Pred. No. 9.6e+02;
                                                                                                                                    0; Mismatches
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                                                                   Query Match
Best Local Similarity 72.1%;
Matches 142; Conservative
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Homo sapiens
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Homo sapiens genomic clone RPCI-11-456H3,
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                                                                                                                                                                                       CTTCCCAGACACTGAGTCTGGAATGAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGG 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                         1928 GGCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATAT 1987
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                                                                                                                                                                                                                                                                                                                                                     234 TAACGGGCTGGTGGGGGGGCTCCACAGGGCCAGTTCAGGGGTTCATCCACAAGAGAGA 293
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 343)

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Map Building
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/clonde lib="RPGT-11"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAG---ATATCTCACCAGCCCTACCTATA
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                                                                1748 GACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCT
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         Gaps
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Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao,
The Institute for Genomic Research
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/mol_type="genomic DNA"
/db_xref="GDB:7674890"
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/clone="RPCI-11-456H3"
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CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Lenght: 8td Error: 0.00
Seq primer: -40nl3 #wd. ET from Amersham
High quality sequence stop: 408.
                                                                                                                                                                                   AA494075 412 bp mRNA linear EST 19-AUG-1997 ng61c08.s1 NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:939278 similar to contains Alu repetitive element;, mRNA sequence.
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/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
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Pred. No. 1.4e+03;
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/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:939278"
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AA494075.1 GI:2223916
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Best Local Similarity 74.8%;
Matches 119; Conservative
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                            1314 TTTTGAAGTAAA 1325
                                                                      471 Trgcaacaraaa 482
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AA494075/c
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                          AQ207760 502 bp DNA linear GSS 18-SEP-1998 HS_3026_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=19 Row=N, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAAC 1194
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                                                                      AAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGTGAAACATTCCATATATT 377
                                                                                                                 522 AAGATTAGCATGGCCCCTGCCCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 463
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
1 117 c 110 g 140 t 5 others
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                                                                                                                                                                                                        scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
191: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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|mol_trype="genomic DNA"
|db_xref="taxon:9606" |
|clone="plate=3026 Col=19 Row=N"
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Plate: 3026 row: N column: 19
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(bases 1 to 315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IntAGE:152701"
/lab_host=="Cone="IntAGE:152701"
/lab_host=="DH10B"
/clone="IntAGE:152701"
/clone="IntAGE:152701"
/clone="DH10B"
/clone="DH30B"
/clone="DH30B"
/note="Organ: pooled; Vector: p7773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Homo sapiens, Similar to hypothetical protein FL/20489, clone
ברימים ברימים ברימים אואם.
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                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dases 1 to 464)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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ol51f11.81 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1527021 3' Eimilar to SW:TSG6 HUMAN P98066 TUMOR NECROSIS
FACTOR-INDUCIBLE PROTEIN TSG-6 PRECÜRSOR ;contains Alu repetitive
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                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (infc@image.llnl.gov) for further information.
Insert Length: 417 Ed Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 345.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .464
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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9
                                                                element;, mRNA sequence
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AA917468.1 GI:3057358
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 73 Row: i Column: 4
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI039619 als bp mRNA linear EST 30-JUN-1998 ox28f05.x1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1657665 3' similar to WP:T20D3.3 CE03672 ;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2772)
                                                                                                                                                          Direct Submission
Submitted (15-COT-2002) National Institutes of Health, Mammalian
Submitted (15-COT-2002) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                         WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
contact: amadame@systemsbiology.org
contact: amadame@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1057 TTCAACTCCTGACCTCAGGTGAACTTCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
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/clone_lib="NHH MGC_95"
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68.9%; Pred. No. 4.8e+02;
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623 c 602 g 865 t
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Matches 144; Conservative
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BF829139/c
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                                                                                                                                                                                                                                                                                                      Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 369)

1 (Dases I to 569)

1 (Dases I, Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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CM3-KT0033-151200-572-£07 KT0033 Homo sapiens cDNA, mRNA sequence.
BF738217
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NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                               Unpublished
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAAATAGGAGCTATACAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                        /organism="Homo sapiens"
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/dev stage="8-9 weeks"
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                                                                                                                                                                        Location/Qualifiers
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Contact: Simpson A.J.G.
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Best Local Similarity 72.2%;
Matches 122; Conservative
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// Organism="Homo sapiens"
/mol type="mRNA"
/db_xref="txxon:9606"
/db_xref="txxon:9606"
/dev stage="Adult"
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/note="Torgan: bladger tumor; Vector: puc18; Site_1: Smal;
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/note="Torgan: bladger tumor; Vector: puc18; Site_1: Smal;
/note="Torgan: bladger tumor; Vector: puc18; Site_1: Smal;
/note="Torgan: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; Vector: bladger tumor; V
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MRI-HN0070-151200-003-h04 HN0070 Homo sapiens cDNA, mRNA sequence.
BF829139.1 GI:12174344
EST.
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1 (bases 1 to 464)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Sogia, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                            Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-KT0033-151200-572-f07&t3=2000-12-15&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence story: 369.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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Pred. No. 1.8e+03;
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85 c 78 g 116 t
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Best Local Similarity 67.3%; Pred. No. 1.8e
Matches 132; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .369
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="wouse 10kb plasmid UUGCIM library"
/note="Westor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                       Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCCAAGAATGACACACAAATTTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530 AGACAAAGCACATAATTANAAATGAGAGTACTGTGCTCGCTTCGGCAGCACATATACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590 AATTGGAACGATACAGAGAAGATTAGCATGGCCCCTGCGCAAGGATGACACGCAAATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 TGAAACATTCCATATATTAAAAATAAATAAATAAAGAGAAAAGGAAAAAA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 reaaccerrecaratritreaaaracaaaarecaaaagcarecraacreaaaa 702
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                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: G column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .723
/organism="Mus musculus"
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                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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Best Local Similarity 71.18
Matches 123; Conservative
                                        Unpublished
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Job time: 4336.79 secs
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84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
/dev_stage="Adult"
/clone lib="MN0070"
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                      Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence acaived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRI&t2=MR1-HN0070-15:100-003-h04&t3=2000-12-15&t4=1)

Seq primer: puc 18 forward

High quality sequence strp: 17

High quality sequence stop: 464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131 TATATATATATAGTATTTGTGGTAGAGATGGGGATTTTGCCATGTTGCCCAGGCTAGTATT 1190
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 723)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 TCCACCCGCCTTAGCTTCCCACAGTGCTGGGATTACAGATAGGTGTGAGCCACCGCGCCC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 GAACTCCTAGGCTCAAGAGATCCACCTCCGCCTCCCAAGTGTTGGGATTACAGGT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ335882 10kb plasmid UUGC1M linear GSS 29-SEP-200 MO065G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0065G12 R, genomic survey sequence.
                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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4.5%; Score 93.6; DB 10; Length 464;
Best Local Similarity 67.9%; Pred. No. 1.6e+03;
Matches 144; Conservațive 1; Mismatches 66; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 GTGAGCCACCGCACCTGGCCAGTTTATTCTTT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                   Brazil
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Gaps

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(USPTO)

Run on:

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1 from Patent WO0246220.
AX468603
AX468603.1 GI:21901402
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5.1 184754
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4.9 219619
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97.6 142902
37.3 229640
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5.0 153899
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Match
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119.6
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ACCESSION
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SOURCE
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AUTHORS
TITLE
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AX468603
LOCUS
                                                       Result
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                                                                           ; Search time 8578.08 Seconds (without alignments) 11245.517 Million cell updates/sec
                                                                                                                                                1 ggatcctttcatgtttaaca......caggtcggaggccaccatgg 2358
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          5.1.6
Compugen Ltd.
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        2888711 seqs, 20454813386 residues
          version 5
                                                                            November 17, 2003, 23:30:20
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Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
                                                                                                                                                                                 Gapop 10.0 , Gapext 1.0
          GenCore (c) 1993
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| htg_hum: *
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Maximum DB
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AL772285 AC091467

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AL663088

AF131883 AL365324

4622

AC022675 AC119697

AC132348 AC102022 AC122205 AL365434

AK468604 Sequence
AF131884 Homo sapi
AK322775 Sequence
BD094076 Shear str
X83703 H.sapiens m
G28603 human STS S
AC074094 Homo sapi
AC122467 Mus muscu
AC132348 Mus muscu
AC132248 Mus muscu
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AC13254 Mus muscu
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AL66568 Mouse DNA
AL662668 Mouse DNA
AL662668 Mouse DNA
AL662668 Mouse DNA
AL662668 Mouse DNA
AL662088 Mouse DNA

AX322775 BD094076 HSRNACINP

AL772175 Mus muscu AC136093 Rattus no AC128045 Rattus no AC123610 Mus muscu AC105665 Rattus no AC128995 Rattus no AC109696 Rattus no AC109696 Rattus no AC109601 Rattus no AC113514 Mus muscu AC116128 Mus muscu AC114123 Mus muscu AC13396 Mus muscu AC13433 Hus muscu AC13396 Mus muscu AC13396 Mus muscu AC13396 Mus muscu

AC109696 AC094069 AC108661

AC116128

0

PAT 16-JUL-2002

linear

DNA

ALIGNMENTS

AX468603 Sequence AC119234 Mus muscu AC105469 Rattus no AC097115 Rattus no BV062893 S212P6025 AF478692 Mus muscu BV076484 S212P6036

AC105469 AC097115 BV062893 AF478692

AX468603 AC119234

ΩB

Description

SUMMARIES

Schwartz, B., Branellec, D. and Chien, K. Sequences upstream of the carp gene, vectors containing them and uses thereof Pred. No. is the number of results predicted by chance to have a

us-10-005-337a-1.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* Gilze: contig of 61126 bp in length

* 61127 142902: contig of 81676 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACTICIGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 others
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/db_xref="taxon:10090"
/clone="RP94-211P24"
/clone lib="RP07-24 Male Mouse BAC"
41376 a 30899 c 29987 g 40473 t 167 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 211_P_24
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Matches 2314;
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Linton, L., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chagelter, B., Brown, A., Canarata, J., Campopiano, A., Chang, J., Chagelter, B., Brown, A., Canarata, J., Campopiano, A., Chang, J., Chagelter, B., Brown, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S. Gord, S., Gord, S., Gordete, M., Illev, I., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Grand-Plerre, N., Landers, T., Lehoczky, J., Levine, W., Illev, I., Johnson, R., Jones, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Methews, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Norbu, C., Norman, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Sewery, P., Spencer, B., Stanges, T., Schupback, R., Strauss, N., Subramanian, A., Tavais, N., Trailio, J., Ve, M., Young, G., Zainoun, J., Zewbek, L., Zimmer, A. and Zody, M. Direct Submission

Nibaret (Submission)

Lirect Submission

Lobam, K., Vo, A., Wilson, B., Wu, X., Wann, D., Ye, W.J., Voung, G., Submitted (15-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                      2101 CTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCT 2160
                                                            1981 ACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTG 2040
                                                                                                                             2041 GTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGCCGCGGCCAG 2100
                                                                                                                                                                                                                                                                                         2220
                                                                                                                                                                                                                                                                                                                 2161 CTGAATTGGCCACTGGTGGGGGGGGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATC 2220
                                                                                                                                                                                                                                                                                                                                                                           TCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGCTCCCACAGGGCCCAGTTCCAG 2280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC119234 142902 bp DNA linear HTG 11-JUN-2003
Mus musculus clone RP24-211P24, *** SEQUENCING IN PROGRESS ***, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 142902)
                                                                                                                                                                                                                                                                                       CTGAATTGGCCACTGGTGGGGGGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATC
                                                                                                                                                                                                                                                                                                                                                                                                         GGGTTCATCCACAAGAGAAAAAAAAATAGACTCGAGGTCTAGGGAGCTTGCATGCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2281 GGGTTCATCCACAAGAGAAAACATAGACTCGAGGTCTAGGGAGCTTGCATGCCTGCA
                                                                                                           GTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGCCGCGGCCAG
                                                                                                                                                                                               CTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAATTCACCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT19234.9 GI:31581760
HTG; HTGS PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-211P24 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCGGAGGCCACCATGG 2358
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VERSION

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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON NOV 15, 2002 this sequence version replaced gi:23101653.
The sequence in this sequence version replaced gi:23101653.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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215567: gap of unknown length
218782: contig of 3215 bp in length
218882: gap of unknown length
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220459: gap of unknown length
221614: contig of 1155 bp in length
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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224871: gap of unbrown 10
225886.
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225986: gap of unknown
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/note="wgs end_extension
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clone end:T7"
complement(7251. .8156)
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/db_xref="taxon:10116"
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                                                                                                                    COMMENT
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                                                     AC105469 229640 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-140118, WORKING DRAFT SEQUENCE, 9
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                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus
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Center project name: GGQJ

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Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Drager, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Branch, C., Friney, M., Flagg, N., Forbes, L., Foster, M., Foster, P., France, C. France, C. M., Garza, M., Garca, A., Garca, A., Garca, A., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Garca, M., Hans, S., Halladn, S.L., Hodgon, A., Hogues, M., Hernandez, R., Howells, S., Hullyk, S., Hume, J., Idlehird, D., Schope, M., Garca, J., Liu, Y., Kaft, C.L., Lebow, H., Levan, J., Levis, L., Li, Z., Liu, J., Liu, M., Liu, Y., Lebow, H., Lozado, R. J., Lu, X., Ma, J., Maheshari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Marcin, K., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., Marcin, R., M
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/fart/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Direct Submission
Submitsed (11-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 238344)
Rat Genome Sequencing Consortium.
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COMMENT

Center: Baylor College of Medicine

Center code: BCM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26418 ATGGAAACCAGAAGGCCAACAGTTGTCCTTCGATAGTGTCTCAGGACAGCCAGGACAGAG 26477
                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                    Consensus quality: 222569 bases at least Q40 Consensus quality: 226638 bases at least Q30 Consensus quality: 229427 bases at least Q30 Estimated insert size: 233018; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26478 ----CACTAGGAGAGAGAACCCACGAAGGA-----TATCAGTGTGCTGGTTTCCAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            879 ATGAAAACGAGAAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 879.8; DB 2; Length 238344;
Pred. No. 1e-245;
0; Mismatches 177; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                236546: contig of 236546 bp in length 236646: gap of unknown length 238344: contig of 1698 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6855 others
Center clone name: CH230-26A2
------ Summary Statistics
Assembly program: Phrap, version 0.990329
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47381 c 49225 g 71429 t
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                                                                                                                                                     GGGGTAGATCCTCTGATTAGCCTTCAGATTTAGAACACGGTGAGCCTGTGGTGCACTAAT 1628
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                           CATGTATCTAGGCAGAT------GCCTATGAATCTCCAGCCTCAAGTGCATGTT
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                                                                                                        AGTIGIGCTICTGCTAAGAACTGGACTCACATCTCTCTGTGCATCACTTCGGCCCGTTTT
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            CGTGTATCTAGGCAGATGCTCTATCATTAGCCCATGAGTCTCCAGCCTCAGACGCACATT
                                                                                                                                                                                                                  ATCAGAAAGATATGGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGATACGTTAGT
                                                          TITICICGGGCTCTCTTAAGCTTT-TCCCACAGCATTGGGAAACTTTACTGACAGCATCCA
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annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

S. Location/Qualifiers

I. 6338

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                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 838) Made, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Landder, E.S., Lindalad-Toh, K. and Daly, M.J. The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
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Pred. No. 5.2e-224;
0; Mismatches 7; Indels 2;
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320 Charles Street, Cambridge, MA 02141, US
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
STS size: 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerstin Lindblad-Toh
Mus musculus (house mouse)
Mus musculus
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BV062893

838 bp DNA linear STS 31-MAY-2003
S212P60252FC3.T0 CZECHII/Ei Mus musculus STS genomic, sequence
tagged site.
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ACCESSION VERSION

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Mammala; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 665)
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.,
Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
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Pred. No. 1.5e-177
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Matches 699; Conservative
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Maeda,T., Sepulveda,J., Chen,H.H. and Stewart,A.F.R.
alpha!-Adrenergic activation of the cardiac ankyrin repeat protein gene in cardiac myocytes
Gene 297 (1-2), 1-9 (2002)
2 (bases 1 to 723)
Maeda,T., Sepulveda,J. and Stewart,A.F.R.
Direct Submission
Submitted (29-JAN-2002) Cardiovascular Institute, University of Pittsburgh, 200 Lothrop Street, Pittsburgh, PA 15213, USA
241
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|product="cardiac_ankyrin_repeat_protein"
|protein_id="AAL85342.1"
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="FVB"
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L. :>723
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/gene="Carp"
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/gene="Carp"
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/gene="Carp"
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BV076484 GI:31192279
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Aventis Pharma S.A. (FR) ; The Regents of The University
California at San Diego (US) ; Benoit, Patrick (FR)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                           as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers
                                                                                                                                                                                                                                                                          WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TCAACTCTCAGCCCCACTTAGCTCTGAGTCAGGCCTGGAACAAACGGCCACAGGAATGAG 300
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                                                                                      Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
structure of variation in the laboratory mouse (6915), 574-578 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 640.2; DB 11; Length Pred. No. 8.3e-176; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="- 19 22-610 35/51955-35751368"
/clone_lib="CZECHII/Ei"
                                                                                                                                         Cambridge, MA 02141, US?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
                                                                                                                                                                     Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
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27.2%;
Best Local Similarity 98.6%;
Matches 656; Conservative
                                                                                                                                       320 Charles Street,
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                                                                                                                                                                                                                   1642 TGTAGGGCATCTACATTTTCTTGATA-GGTAGTCATATGAAAGCTGACAAAGAA--AAAA
                                                                                                                                                                                                                                                                        CCATCTCCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTC
                                                                                                                                                                                                                                                                                                                              CCAGCCAACTGGAGTGCTGATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATG
                                                                                                                                                                                                                                                                                                                                                                                   1898 CACAGTGC - TIGCATITICITICATACGTTAGTCATATGAGAGCTGACAAAGAAGGAAAA
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                                                                                                        TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAGT
                                                                                                                         1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGATGTTT
                                                     1540 TCTCTCTGTGCATCACTTCGGCCCGGTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                            22;
  Length 2074;
                            Indels
Score 367.8; DB 9;
Pred. No. 5.9e-96;
0; Mismatches 162;
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ALS90622
ALS90622.
HTG; CARP; ribonuclease P
Homo sapiens (human)
Homo sapiens
 15.6%;
larity 76.4%;
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nes 597; Conserv
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                                                                             1758 AIGACTIGCATIGCTGAGCGAIGTGACCACCAAGGAATGGCCCTCTCACATITCTT 1817
                                                                                                                                     TGACTTGGCTTCCCAGGCTGGAAGATTATCTCAGCCCTAGCTATATAA-CGGGCTG 2249
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                                                                                                                                                                                                                                             Anhar, Y.
Direct Submission
Submitted (26-FEB-1999) Second Department of Internal Medicine,
Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 2074)
Aihara, V., Kurabayashi, M., Tanaka, T., Sekiguchi, K., Tomaru, K., Kanai, H., Takeda, S. and Nagai, R.
Human CVARP S'-flanking region
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="cardiovascular-specific cardiac ankyrin repeat
                                                              2016 ATGACTCGCATTGCTGAGCGGTGTCGTCACTGCCAAAGGAATGACCCTCTCACATTTCTT
                                                                                                                    CCTGATTCGCATACGCCGCGG-----CCAGCTTGTCATCTCCCCTCTTGGGCTTCCCAGAC
                                                                                                                                                                         ACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCAGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .2074
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1. _1832
/note="5'-flanking region"
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/gene="CVARP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF131884.1 GI:6940841
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/gene="CVARP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="CARP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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/tränslation="MAVFADLDLRAGSDLKALRGLVETAAHLGYSVVAINHIVDFKEK
KQEIEKPVAVSELFTTLFIVQGKSRPIKILTRLTIIVSDPSHCNVLRATSSRARLYDV
VAVFPKTEKLFHIACTHLDVDLVCITVTEKLPFYFKRPPINVAIDRGLAFELVYSPAI
                                                                                                                                                                                                                      KDSTMRRYTISSALNIMQICKGKNVIISSAAERPLEIRGPYDVANLGLLFGLSESDAK
AAVSTNCRAALLHGETRKTAFGIISTVKKPRPSEGDEDCLPASKKAKCEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 13. .262 of consensus"
complement(4176 ..4649)
/note="match: GSS: Em:AQ626500"
join(<4648. .4764,7467. .7538,14216. .14305,23179. .23887,
24284. .24321,44717. .24796,28974. .29381)
                       /evidence=not_experimental
/product==hba320F15.1.1 (ribonuclease P (30kD) (RPP30))"
/protein_id=='AAC70100.1"
/db_xref="GI:15717970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="1.2 repeat: matches 1808 .1971 of consensus" 5440 .5721 /note="AluSx repeat: matches 7 .293 of consensus" 5722 .6337 /note="1.2 repeat: matches 1200 .1808 of consensus" 6884 .7196 /note="AluJb repeat: matches 1 .312 .0f consensus" /note="AluJb repeat: matches 1 .312 .0f consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="L2 repeat: matches 2423. .2481 of consensus"
                                                                                                                                                                                                                                                                                                                                                                    .2502 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2732 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .282 of consensus"
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/note="AluSx repeat: matches 1. .289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 16. .112 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .212 of consensus"
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note="HY1 repeat: matches 1. .42 of consensus"
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note="match: ESTs: Em:AW939965"
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2939. .3167
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16979. .17036
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257. .5439
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                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 2459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ805524"
1907, .2434
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                                                                                                                                                                                                                                                                                   189. .800
'note="MIR repeat: matches 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roce="match: GSS: Em:AQ775672"
1926. .2208
"Gene="bA320F15.1"
froce="match: GSS: Em:B92129"
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1086, 11219
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                                                                                                                                                                                                                                                                                                                                                                                                            gene="bA320F15.1"
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/gene="bA320F15.1"
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join(391. .472,3273. .3328,3962. .4018,4428. .4502,7467. .7538,
4216. .14305,23179. .23295,23858. .23887,24284. .24321,
24717. .24796,28974. .29083)
gene="ph320F15.1"
/note="match: proteins: Tr:P78346 Tr:088796"
                                                                                                                            Submitted (19-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Cubmitted (19-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk

On May 31, 2001 this sequence version replaced gi:14161205.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORWEPP; Information on the WORWEPP
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14216. .14305,23179. .23255,23858. .23887,24284. .24321,
24717. .24796,28974. .29381)
/gene="bA320F15.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RPI1-320F15 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RPI1-236B18 is at 50012 in this
sequence. The true right end of clone RPI1-103A2 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-320F15 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="march: CDNAs: Em:U77665 Em:AK004137 Em:U95123
match: ESTS: Em:BE72689 Em:BE378859 Em:BE137893
Em:AA920575 Em:BG106820 Em:BF681617 Em:BF248001
Em:BP031745 Em:AA854455 Em:A1359795"
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complement(1. .98)
/note="match: GSS: Em:AQ670367"
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//note==match: 058: Em:AQ544636"
complement (1. .77)
/note="match: STS: Em:G56439
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/db_xref="taxon:9606"
/chromosome="10"
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/gene="bA320F15.1"
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Direct Submission
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49633 CAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGTGG 49574
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                                                                                                                                                                                                                    GGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CG 2244
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                                                                        TICITCCTGATICGCATACGCCGCGG-----CCAGCTIGICATCTCCCTCTTGGGCTTCC
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     GTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACAT
                          49753 ATAGGATGACTTGCATTGCTGAGGGATGTGATCACCACCAAAGGAATGGCCCTCTCACAT
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Novel target genes for diseases of the heart
Patent: WO 0192567-A 19 06-DEC-2001;
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AX322775
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1. 1901
/organism="unidentified"
/orl_type="genomic DNA"
/db_xref="taxon:32644"
a 378 c 460 g 471
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BD094076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50106 AAAGTGCATTACTGAATGCTTTCAATTTCTTATAATGATGGTAGCATGTCATGTGGG 50047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49986 AGGCCCCATCCCTTCAGGCTGTTACCCAGGGAATAGGATGTCC---TGGGAC 49930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACC 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1773 CAGACCCATCTCCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAAC 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGCACAGTGC--TTGCATTTTCTTGATACGTTAGTCATATGAGAGCTGACAAAGAAG 1950
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                                                                                                                                                                                                                                                                                                    /product="bA320F15.1.3 (putative isoform 3)"
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Em:BF435407 Em:A1740881 Em:AA651912 Em:BF438915"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 45. .304 of consensus" 19198. .19363 / note="LIME repeat: matches 5272. .5435 of consensus" 19489. .19928 / note="MITIC repeat: matches 5. .478 of consensus" 21838. .22258 / note="LZ repeat: matches 2109. .2669 of consensus" / note="LZ repeat: matches 2109. .2669 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28442. .28516 -
/note="L2 repeat: matches 2636. .2710 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .133 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.7%; Score 347.6; DB 9; Length 50111; Best Local Similarity 78.2%; Pred. No. 7e-90; Matches 521; Conservative 0; Mismatches 129; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ223714"
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/note="match: GSS: Em:AQ551877"
1709. .17972
                                                                                                                                                                                                22440. .22946
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/gene="bA320F15.1"
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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/db_xref="SPTREMBL:Q15327"
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CLEGHLAI VEKLMEAGAQ I EFRDMLESTA I HWA SRGGNLDVLKLLLNKGAKI SARDKL
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DLNIKNCAGKTPMDLVLHWQNGTKAIFDSLRENSYKTSRIATF"
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human STS SHGC-35401, sequence tagged site.

228603.
G28603.1 G1:1408418
STS; STS sequence; primer; sequence tagged site.
Homo sapiens (human)
Homo sapiens
Eukkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La Roche, Nutley, NJ 07110, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TCCCCTCCCTCTTCAGCTTCCCAGACACTGATTCTGGAATGAAATTCACCTGCCTCTGA
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nuclear protein from human endothelial cells
J. Biol. Chem. 270 (17), 10236-10245 (1995)
95247734
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/note="nuclear localization signal"
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/note="ankyrin-like repeats"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="endothelial"
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ACCESSION
VERSION
KEYWORDS
SOURCE
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MEDLINE
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TITLE
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Daese 1 to 1901)
Nojima, H., Yoshisue, H., Obayashi, M., Ota, T., Kawabata, A., Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S. Shear stresponsive DNAS
Patent: WO 0125427-A 37 12-APR-200;
KYOWA HAKKO KOGYO CO LTD, HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBSYASHI, TOSHIO OTA, AYAKO KAWABATA, KAZCHIRO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO
OS HOMO sapiens (human)
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02-OCT-2000 WO 2000JP006840
01-OCT-1999 JP 99P 280976
HIROSHI NOJIMA,HAJIME YOSHISUE,MASAYA OBAYASHI,TOSHIO OTA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 GTTGGCTCCTAATGGGGGTGGGGGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCAC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 recertécéretres de recensor de la recensor de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recente de la recent
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Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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H.sapiens mRNA for cytokine inducible nuclear protein.
X83703
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Pred. No. 6.9e-26;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db stref="taxon:9606"
a _378 c 460 g 471
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Homo sapiens
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source

FEATURES

BASE COUNT ORIGIN

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Gaps

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STS 11-JUL-1996

DEFINITION ACCESSION VERSION

RESULT 13 HSRNACINP

KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

us-10-005-337a-1.rge

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The sequence of Homo sapiens clone Unpublished
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                                            AC074094,
AC074094.3 GI:9958197
HTG5, HTG5_PHASE1, HTG5_DRAFT.
Homo sapiens (human)
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13497: gap of
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                                                             VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2165 ATTGGCCACTGGTGGGGGCGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prepared with primer pairs provided by Sandoz, derived from X83703
-- Washington University/Merck EST sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                     seconds
seconds
seconds
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82.6%; Pred. No. 6.9e-26;
tive 0; Mismatches 34; Indels 2;
                                                                                                                                                                                                                                      Initial incubation: 94 degrees C for 90 seconds
                                                    Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
                                                                                                                                                                                                                                                                    94 degrees C for 15 s
62 degrees C for 23 s
72 degrees C for 30 s
30
                                                                                                                                                                                                                                                                                                                              Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                           25 ng
each 1 uM
each 200 uM
0.05 units/ul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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1 378 c 460 g 4
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Primer B: CCAGATGGATGATCATGAAGG
STS size: 222
PCR Profile:
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                                                                                                                                                Email: myers@shgc.stanford.edu
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50
20
8.3
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Annealing:
Polymerization:
PCR Cycles:
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Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                Thermal Cycler:
1 (bases 1 to 1901)
Myers, R.M.
Unpublished (1996)
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1246. .1263
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Best Local Similarity 82.6'
Matches 171; Conservative
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REFERENCE
AUTHORS
JOURNAL
COMMENT
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ncu/4094 160350 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 10 clone RP11-236B18, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                               To Chaese 1 to 160350)
Waterston, R.H.
Direct Submission
Submitted (13-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:9665205.
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160350)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
Center code: WUGSC
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unknown length
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of 1355 bp in length
unknown length
of 1655 bp in length
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113707 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAATGCTCCAATTATTATGCTGTT 113648
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52.5%; Pred. No. 2.9e-25;
tive 0; Mismatches 153; Indels 2;
150852: contig of 3466 bp in length
150952: gap of unknown length
153550: contig of 2598 bp in length
153650: gap of unknown length
15757: contig of 3607 bp in length
157357: gap of unknown length
160350: contig of 2993 bp in length
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note="assembly_name:Contig12"
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note="assembly_name:Contig15"
0234. .68088
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.3498. .141732
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11833. .143187
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|3288. .144942
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47387. .150852
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:0953. .153550
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57358. .160350
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13651. .157257
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32724 c 33135 g 45498 t
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/organism="Homo sapiens
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Search completed: November 18, 2003, 04:21:58 Job time : 8596.58 secs

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protein; CARP; cardiant; immunosuppressive; therapy; antisense gene therapy; mouse; ds.
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(c) 1993
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Score

Result 8

The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament intended for the treatment of cardiac insufficiancy, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac cardiac correcting muscle contractility. (IIb) is useful for expressing a gene of therapeutic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is expressed. (I) the vectors and the compositions are useful in clinical, expressed. (I) the vectors and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac prevention of cardiac pathologies. (I) is also useful for generating molecules for their activity on the regulatory sequences of the gene encoding the CARP protein. The prasent sequence represents the DNA fragment upstream of the coding sequence of a mouse CARP protein. sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells 1; Fig 1; 48pp; English Claim 

Sequence 2358 BP; 636 A; 567 C; 542 G; 613 T; 0 other;

480 540 540 120 120 180 180 240 240 300 360 360 GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG 420 420 480 9 9 09 CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATATATTTAT GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG rgtgaaactcagcccatccca GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCA 121 ACACTICIGCAAGCCCCAICCICIACAAGGGCTCAITGGGAATTICCIGGAGCTICIC TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGG CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATTATAT GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCATTCTTCAAAGTGATGTGTTCACA ACACTTCTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCATTCTTCAAAGTGATGTGTTCACA Gaps Ouery Match 100.0%; Score 2358; DB 24; Length 2358; Best Local Similarity 100.0%; Pred. No. 0; Msmatches 2358; Conservative 0; Mismatches 0; Indels 0; GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTT 61 61 181 181 241 301 301 361 541 121 241 361 421 421 481 g В ò 8 ò 유 ò ద ò 8 B G Š ద ð. 음

1680 1020 1020 1080 1080 1140 1200 1260 1260 1320 1380 1380 1440 1440 1500 1500 1560 1560 1620 1620 CCCTAATTAACACTTCCCTCTTCTACTGACACCCCTTCACTCTCCTCTTTCATAAAAA 1200 960 096 900 099 99 720 720 780 780 840 840 900 900 TGGAAGGGTGAGGAGAGAGACAGATATATGATGGCCAGCATAACAAAACATACACAACA TTTTGCCTCTCTCAACAGCAAAGCTTGGGGCCCTTTTTGTTTCCTTTAGGAATAGAACA CGAGAGCCCCGTGTATCTAGGCAGATGCTCTATCATTAGCCCATGAGTCTCCAGCCTCAG ACGCACATTTTTCTCGGGCTCTTTAAGCTTTTCCCACAGCATTGGGAAACTTTACTGAC CTTGTCACTTCAAGAGGTCAAAGAAATAGTGTTAACCATGAAAAGGAGAGGACGACAACAG CACGAAGGACAAGGTATTAGTGTTTTGTGTTTTCAGGGCAATGTCTTGTACTGAAGATTCT CCCTAATTAACACTTCCCTCTTCTACTGACACCCCCTTCACTCCTCTCTTTCATAAAAA TAAAAAAAGTATTTTATGTGGCTCTTACGATAGAATCTTTCCTCGAACTATAAAAAGATC TAAAAAAAGTATTTTATGTGGCTCTTACGATAGAATCTTTCCTCGAACTATAAAAAGATC CGAGAGCCCCGTGTATCTAGGCAGATGCTCTATCATTAGCCCATGAGTCTCCAGCCTCAG AGCATCCAAGTTGTGCTTCTGCTAAGAACTGGACTCACATCTCTCTGTGCATCACTTCGG GCACTAATTATGGCCAGTGACACCATAGAGTCCAAAGTGCATTACTGAATGCTTTCAATTT CACCTICTAGCTCTGCATCCATAGCAAGTAGCCTAATGTTTCTGTGTCTAGGTGTCATCT TTAGCTCTGAGTCAGGCCTGGAACAAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTG TTAGCTCTGAGTCAGGCCTGGAACAAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTG TTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAGAGAACACTAGGAGGGGGAACC TAAATATTTATATTTTCACATTTTAATATCTTAGCGATGACAAGCCAGAAACAAGTATT 1261 TAAATATTTATATTTTTTCACATTTTAATATCTTAGCGATGACAAGCCAGAACAAGTATT TTTTGCCTCTCTCAACAGCAAAGCTTGGGGGCCTTTTTGTTTCCGTGTTAGGAATAGAACA CCCGTTTTGGGGTAGATCCTCTGATTAGCCTTCAGATTTAGAACACGGTGAGCCTGTGGT CTGTGAATCGAGATCCTTGGCCTTGCTTGAATTAGGGAGGCACAAAATACTCAGAGATTC AAGACTGCTCAGCAGCCCCAGAGTCCTTCCTCAAAGGAAAGGTCTCAACTCTCAGCCCCCC AAGACTGCTCAGCAGCCCAGAGTCCTTCCTCAAAGGAAAGGTCTCAACTCTCAGCCCCCC CACGAAGGACAAGGTATTAGTGTGTTGGTTTTTCAGGGCAATGTCTTGTACTGAAGATTCT AGAAACACAATTTGCTGGTTGAACAGCTGAAGTGGGGGTGGGGGTTCTTACCCCATGTTCA cccgrrrrgcccradarccrcrcarracccrrcacarrracaacaccccrcaccrcaca CACCTTCTAGCTCTGCATCCATAGCAAGTAGCCTAATGTTTCTGTGTGTCTAGGTGTCATCT 1441 1561 1021 1081 1081 1141 1141 1201 1201 1261 1321 1321 1381 1441 1501 1501 1561 1621 601 841 841 901 196 1021 1381 541 601 661 661 721 721 781 781 901 961 ò d 8 ò g ò g ò g ò Db ò g  $\delta$ g 8 B 8 g ò g ò a ò 유 õ 8 ò g ò g ò g ò

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1621 GCACTAATTATGGCCAGTGACACCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTT 1680
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                                                                             TTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTCCCAGCCAACTGGAGTGCTGATAA
                                                                                                                    GTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGAT
                                                                                                                                            ACGTTAGTCATATGAGAGCTGACAAAGAAGGAAAAAAGAGCAGCGATGTGGTGCAATATTA
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                                                                                                                                                                                                                                                                                                                                     cardiac ankyrin repeat protein (CARP) promoter.
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The invention relates to a human type-5 recombinant adenovirus vector for achieving cardiac-restricted transcription of a gene of interest. The vector comprises inverted terminal repeat (ITR) sequences from human adeno-associated virus (AAV) type 2 (AAAI0405) and a cardiac tissue-specific promoter. In particular, the promoter is that of the cardiomycoyte-restricted cardiac ankyrin repeat protein (CARP) gene. The adenovirus vector is used for targetted gene therapy for heart disease and for evaluating gene function. Cardiac restricted transcription of a transgene in both neonatal and mature cardiac tissues can be achieved to treat inherited and acquired heart diseases. The vector is suitable for tissue-specific use in vivo and in vitro and provides cardiac restricted transcription. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents the murine cardiac ankyrin repeat protein (CARP) promoter
                                                                                                                                                                                                                        Human type-5 recombinant adenovirus vector used for targeted gene therapy for heart disease and evaluating gene function contains a tissue-restricted promoter and inverted terminal repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.8%; Score 1763.4; DB 21; Length 2247; Best Local Similarity 91.2%; Pred. No. 0; Matches 2124; Conservative 0; Mismatches 69; Indels 137;
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                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 29-30; 33pp; English
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The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament in tended for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility. Cardiac hypertrophy, cardiac of the cardiac correcting correcting contractility. (IIb) is useful for expressing a gene of the cardiac interest in vivo, by isolating (IIb) and introducing (IIb) in the vectors and the compositions are useful in clinical, expressed (I), the vectors and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating cranspenic animals which constitute models for studying certain cardiac prevention of pathologies. (I) is also useful for screening concluding the CARP protein. The present sequence represents the DNA fragment upstream of the coding sequence of a human CARP protein.
                                            New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells
                                                                                                                                                                                             Claim 5; Fig 2; 48pp; English
WPI; 2002-740642/80
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Sequence 2074 BP; 612 A; 469 C; 416 G; 572 T; 5 other;

2075 1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT 1348 1898 CACAGTGC--TTGCATTTTCTTGATACGTTAGTCATATGAGAGCTGACAAAGAAGAAGAAAA 1955 1657 1405 GCATTACTGAATGCTTTCAATTTCTCCTAATGCTACGATGGCATGTCACAGGGCCAT 1717 1718 TTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCAGAC 1777 CCATCTCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTC 1837 1838 CCAGCCAACTGGAGTGCTGATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATG 1897 1585 C---CTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAAGATATTACTGGGGGTGTGATA 1641 1642 TGTAGGGCATCTACATTTTCTTGATA-GGTAGTCATATGAAAGCTGACAAGAA--AAAA 1698 1699 AGGGCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAATAGG 1757 1758 ATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTT 1817 1525 cchgarccerrcecercagecrerrracceaggaaraggargreerggacaagaerree 1584 1598 TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAGT 1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT ATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTT Gaps Score 367.8; DB 24; Length 2074; Pred. No. 5.9e-97; 0; Mismatches 162; Indels 22; Query Match 15.6%; Best Local Similarity 76.4%; Matches 597; Conservative 1658 1466 1778 Query Match 셤 g ò g 8 g ò g ò g ò qq 8 g g δ ò ò

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                                                                                                                                                                                                                                                                                                                                 1938 TTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCG 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaenia; nervous system disorders; arthritis; inflammation; ss.
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                                                              TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                   GTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATAG
                                                                                                                               ACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 13568.
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18-MAY-2000; 2000US-0577409.
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'note= "AU-rich mRNA decay element"
Pred. No. 1e-26;
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/note= "AU-rich mRNA decay
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/note= "66268 cDNA f
1604.1753
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/note= "AU-rich m
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/note= "SIMC01-1
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             82.6%;
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                                                            2105 TCATCTCCCTCTTGGGC
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/product=
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             Best Local Similarity 82.6
Matches 171; Conservative
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           but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                     87 GTTGGCTCCTAATGGGGGGGGGGGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCAC
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                                                                                          DB 22; Length 1988;
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Pred. No. 3.6e-27;
0; Mismatches 33; Indels
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                                                         Sequence 1988 BP; 632 A; 384 C; 472 G; 500 T; 0 other;
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Sugano S;
                          at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                           207 TTCCTTC-CACGACAGAAAACATACA
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Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH02910 standard; DNA; 1901
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                                                                                         Query Match 5.5%;
Best Local Similarity 83.1%;
Matches 172; Conservative
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P-PSDB; AAB90787.
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           specification,
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Kuga T,
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the present sequence to that the grace antername and the present sequence to the murine gastrokine group, designated antrum mucosal protein 18 (AMP-18). AMP-18 was initially detected in mammalian gastric antrum mucosa by a differential screen of CDNA libraries obtained from different regions of the pig stonach. A CDNA was also isolated from a mouse library (see ABZ24608). Genomic AMP-18 DNA sequences were subsequently cloned as a prelude to the analysis of gene regulatory elements. AmP-18 protein is expressed at high levels only in the gastric antrum, and is synthesised in the lumenal sufface mucosal cells. Partially purified AMP-18s from mouse and pig antrum tissue are mitogenic to confluent stomach and kidney epithelial cells in culture. This effect is inhibited of y specific antisera, suggesting that AMP-18, role in the repair of the stomach epithelium following damage by agents such as alcohol. Conservice by protein and reconstruction and reconstruction and reconstruction following damage by agents such as alcohol. Conservice principle of AMP-18, cancers. AMP-18 protein, or an active peptide of AMP-18, is used in a claimed method of stimulating the growth of epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastric Antrum Mucosal Protein 18, useful for preparing a composition for healing of the injured gastrointestinal tract
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 tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. The method useful to treat disease of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardionomyopathy, specific heart muscle disease, thythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial hypertension, pulmonary heart disease, valvular heart disease, congential heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart diseases. The present DNA sequence is expressed sequence tag
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                             Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
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                                                                                                                                       The patent discloses novel target genes abnormally expressed in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrokine; AMP-18; gastric antrum mucosal protein; mitogen; factor; vulnerary; antiulcer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 128.6; DB 24; Length 1901;
Pred. No. 1e-26;
0; Mismatches 34; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1874

/*tag= a

1945..6542

/*tag= b

/product= "Mouse pre-AMP-18"

/note= "contains introns"
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                                                                                                        Claim 2a; Fig 10b; 154pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.8
Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
P-PSDB; AAE16633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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growth
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Agarwal K;

Powell CT,

Walsh-Reitz M;

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Protein inhibitor, useful for treating gastrointestinal disorders or diseases comprises isolated homologous cellular stimulating proteins
                                                                                                                                             Disclosure; Fig 4; 84pp; English.
                                           29-MAR-2002; 2002WO-US09885.
                                                          29-MAR-2001; 2001US-0821726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BANY ) BANYU PHARM CO LTD.
                                                                                         Martin TE,
                                                                          (UYCH-) UNIV CHICAGO
                                                                                                        WPI; 2003-103239/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003004637-A1
               WO200278640-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug
                             10-OCT-2002
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                                                                                         Poback GF,
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                                                                                               TT-ACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAAC 316
                                                                 198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCCT
                                                   Gaps
                                                                                                                                                                                                                                             protein; gastric antrum mucosal protein; gastro-intestinal disorder; cell therapy;
                                                   ë,
                                                                                                                             AGTAGCAAAATTACAGGTATGAAATAGCAATGAAATTATTATGATTG 365
                                                                                                                                             557
                                   4.0%; Score 95; DB 25; Length 7280; 80.5%; Pred. No. 1.6e-16; ive 0; Mismatches 30; Indels
                                                                                                                                          AGTAGCAAAATT -- AGTTAGGAAGTAGGAACAAAATAACGTTATGGTTG
                    Sequence 7280 BP; 2131 A; 1597 C; 1606 G; 1944 T; 2 other;
     cells in the gastrointestinal tract.
                                                                                                                                                                                                                                                                                   ocation/Qualifiers
906..1956
                                                                                                                                                                                 AAD50815 standard; DNA; 7280 BP
                                                                                                                                                                                                                                            Cellular growth stimulating gastrokine; AMP-18 protein;
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/number= 2
3673..3813
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/number= 3
4595..4705
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4706..5607
/*tag= h
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/number= 6
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/*tag= j
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                                                                                                                                                                                                              (first entry)
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                                          Best Local Similarity 80.5
Matches 136; Conservative
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                                                                                                                                                                                                                              Mouse pre-AMP-18 gene
                                                                                                                                                                                                                                                            ulcer; mouse; ds.
                                                                                                                                                                                                              02-APR-2003
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                                   Query Match
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The invention relates to a protein inhibitor which comprises homologous cellular growth stimulating proteins designated gastrokines. The invention also provides gastric antrum mucosal proteins designated AMP-18 which belongs to the novel group of gastrokines and nucleic acid molecules encoding such proteins. Pharmaceutical composition comprising growth stimulating peptide derived from a gastrokine protein is useful for treating gastro-intestinal disorder or diseases associated with overgrowth of gastric-intestinal disorder. The invention is useful in cell therapy. The present sequence is mouse pre-AMP-18 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 TT-ACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTGGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition; food intake disorder; body weight disorder;
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س
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 7280;
                                                                                                                                                                                                                                                                                                                                      Sequence 7280 BP; 2131 A; 1597 C; 1606 G; 1944 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.0%; Score 95; DB 25;
Best Local Similarity 80.5%; Pred. No. 1.6e-16;
Matches 136; Conservative 0; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           histamine receptor H3; anorectic; gene; ds.
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ABZ82337/c
ID ABZ82337 standard, DNA; 18105 BP.
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Kotani

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208887 GGGTCACAGATACCCTGAATGTTGCATATTTATATTACAATTCATAGCAGCTGCA 208946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208828 GCAGCAGTTCCCAACGTGTGGGTCCAATCTCTTTGGGAG-CCCAAAGGCCCTTTCACAG 208886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a DNA molecule that directs neuron-specific transcription of a promoter segment in a mammalian cell. The promoter segment is from the mouse genomic Presenilin-1 gene. Transgenic non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 AAATTACAGGTATGAAATAGCAATGAAATTAATTTTA----TGATTGAAGGTCACACAA 379
                                                                                                                                                                                                                                                                                                  Sequence 659158 BP; 177521 A; 147222 C; 149414 G; 184754 T; 247 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  204 GCAGCAGTICTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCCTTTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 GGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCA
The invention describes an isolated nucleic acid molecule encoding
               gene product that, when knocked out, results in a high growth (hg) phenotype. For example a nucleic acid disrupting the Socs2 gene is unseful for producing an animal characterised by a hg phenotype, by inhibiting expression of Socs2 (supressor of cytokine siganling 2) gene. The nucleic acids of the invention are useful for regulating body size in mammals. gene. The nucleic acids of the invention are useful for regulating body size in mammals. This sequence represents the mouse high growth region.

Note: This sequence did not form part of the printed specification but, was obtained in electronic format directly from the US patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuron-specific transcription; promoter; mouse; Presenilin-1 gene; transgenic; laboratory model; Alzheimer's disease; ss.
                                                                                                                                                                                                                                                                                                                                               Length 659158;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                           Query Match 3.8%; Score 88.8; DB 25; Best Local Similarity 74.7%; Pred. No. 1.3e-13; Matches 139; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                          segdata.uspto.gov/seguence.html?DocID=20020155564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 51-81; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX55300 standard; DNA; 48974 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0920422
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                                                                                                                                                                                                                                   office at
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                                                                                                                                                                                                        The invention relates to novel drug compositions for the treatment and prevention of disorders of food intake and body weight containing as the active component histamine receptor H3 protein, or DNA encoding it, or an agonist to it. A composition of the invention has anorectic activity. Compositions containing the histamine receptor H3 protein may be used in the treatment and prevention of disorders of body weight and food intake. The present sequence represents the mouse histamine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10825 CAACCCCTTTGGGGGGCTCACATATCAGATATCCTGCCTATCAGATGTTTATACTGTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTACAGTAGCAAAATTACACTTATGAAGTAGCAACAAAATAATTTTATGGTTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene that when downregulated or knocked-out, results in high h phenotype, useful for regulating body size in mammals e.g. t, bovine and canine -
                                                                                                   Histamine receptor H3 protein and its agonists and antagonists for treatment and prevention of body weight and food intake disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.8%; Score 89.2; DB 25; Length 18105; 79.1%; Pred. No. 1.3e-14; ive 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18105 BP; 3981 A; 5123 C; 4944 G; 4041 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High growth region; high growth phenotype; Socs2; body size; supressor of cytokine signaling 2; ds; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 18; 49pp; English
                                                                                                                                                                    Example 1; Page 53-65; 73pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX16390 standard; DNA; 659158 BP
                  Ξ,
                    Suwa
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                  Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
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                                                      WPI; 2003-221596/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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rodent,

growth

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RESULT 10
ABX16390
ID ABX16390
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Seguence 707 BP; 205 A; 174 C; 156 G; 169 T; 3 other;
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                                                                                                                                                                                                                                                                                      15325 A-CCTTTTCACAAGGGTCACACATCAGAGATCCTGCATATCCGATATTTATGTTATGATT 15267
                                                                                                                                                                                                                                                                                                                                         15385 GCTACACTCTAGATCGGTGGTTCTCAAGCTGGGGGGTCGCGACCCCTTTGGGGGTTGGACA 15326
                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method used for evaluating the toxicity of an agent comprising determining the expression of a rat toxic response gene(8) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and analysis before a new drug or compound is approved for human consumption or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in
                                                                                                                                                                                                                                                     251 CGACCCTTTACAGGGGTCACATATCATCTATATGTGTGAGGTATTTACATTACGATT
                                                                                                                                                                                     191 GCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAA
                                                                                                                                                                                                                                                                                                                        CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxicity study; rat toxic response gene; toxicological response; development; phase-1 rat CT gene; ds.
                                                                                                                                                     Gaps
     comprising the neuron-
 mammals containing a DNA expression cassette comprising the neuron-
specific promoter are useful as laboratory models for studying the
function of the Presenilin gene, and for studying the etiology of
                                                                                   Sequence 48974 BP; 12579 A; 10749 C; 11189 G; 14438 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluating the toxicity of an agent, useful in drug development
                                                                                                                    Length 48974;
                                                                                                                                                     7;
                                                                                                                   Score 88.6; DB 20; Length
Pred. No. 3.5e-14;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 155; 388pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phase-1 Rat CT gene SEQ ID No 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Farr SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                       15206 CACCATGACATGAAG 15192
                                                                                                                                                                                                                                                                                                                                                                                        371 CACCACAACATGAGG 385
                                                                                                                   Query Match 3.8%;
Best Local Similarity 69.2%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT09109 standard; DNA; 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2001; 2001US-264933P.
26-JUL-2001; 2001US-308161P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response to the test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
containing a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hicken SH,
                                                  Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-674961/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200266682-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                                                                                        311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug
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                                                                                                                                                                 292 ACCCCTTTGGGGGTTAAATGACCCTTTCACATATCAAATATCAAATACCTGCAG 351
                                                                                                                                                                                                                        352 AGCAGATATTCACATTGCAATCCGCAACAACAGCAAAATTACAGTTACGAAGTAAGCAAAG 411
                                                                                                   232 GAGCCATCCCTCCAGCCCCAGCCTGTTTTTATGGAAGTGATTCTCAACTCATGGGTCATG
                                                                                                                                  231 ACCCCTTTGGGGG--AATCAAACGACCCTTTACAGGGGTCACATATCATCTATAT
                                                                                                                                                                                                    289 GTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATG
                                                                   GAGCTTCTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCG
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated nucleic acid molecule encoding gene product that, when knocked out, results in a high growth (hg) phenotype. For example a nucleic acid disrupting the Socs2 gene is useful for producing an animal characterised by a hg phenotype, by inhibiting expression of Socs2 (supressor of cytokine siganling 2) gene. The nucleic acids of the invention are useful for regulating body size in mammals. gene. The nucleic acids of the invention are useful for regulating body size in mammals. This sequence represents the mouse high growth region.

Note: This sequence did not form part of the printed specification but was obtained in electronic format directly from the US patent
                                  3
   707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene that when downregulated or knocked-out, results in
h phenotype, useful for regulating body size in mammals
t, bovine and canine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High growth region; high growth phenotype; Socs2; body size; supressor of cytokine signaling 2; ds; mouse.
   Length
                                  Indels
                                                                                                                                                                                                                                                                   349 -AAATAATTTTATGATTGAAGGTCACCACAACATGAGGCC 387
                                                                                                                                                                                                                                                                                      DB 24;
.9e-14;
es 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      segdata.uspto.gov/sequence.html?DocID=20020155564
                                  0; Mismatches
 Score 83.6;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 18; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horvat S;
                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                 ABX16390 standard; DNA; 659158
3.5%;
ilarity 67.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0999477
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse high growth region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradford E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
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             Best Local Similarity
Matches 148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002155564-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2002
                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                     ABX16390;
   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp
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3 256

Gaps

3.4%; Score 80.4; DB 24; Length 10917; 70.8%; Pred. No. 3.9e-12; ... ive 0; Mismatches 51; Indels 5;

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197 ITCTAGGGCAGCAGCAGTTCTCAACCTGGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCC
   useful for monitoring the efficacy of a drug against depression.
                                      Sequence 10917 BP; 2423 A; 2842 C; 2929 G; 2706 T; 17 other;
                                                                     Query Match
Best Local Similarity 70.8°
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV06155;
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                                                                                                                                                                                                         439358 Tr.-CTGCGTAGCATATCAGACATCCTGCATATCAGATATTTCCATTATGACACATAATG 439301
                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the genomic DNA sequence of the wild-type mouse Wolfram Syndrome 1 (WFS1) gene used in the method of the invention. The specification describes a non-human transgenic mammal comprising a genome containing a single copy of a wild-type WFS1 gene and a modified WFS1 allele containing a must disrupts the function of wolframin, or its transgenic progeny. Wolframin is a predicted transmembrane protein expressed in many tissues including pancreas and brain. The transgenic nonhuman animals are useful as models for depression, particularly as models for depression in humans. The animals exhibit chronic stress-induced neurochemical and behavioural changes associated with depression. The transgenic animals are also useful for screening or identifying antidepressant agents, drugs or genes that may be employed to ameliorate or treat depression. The animals are also
                                                                                                        198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT 257
                                                                                                                                                                          258 TTACAGGGGTCACATATCATCTATACTATATGTCAGGTATTTACATTACGATTCGTAACA 317
                                                                                                                                                                                                                                               318 GTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGATGAAGGTCACCACA 377
Sequence 659158 BP; 177521 A; 147222 C; 149414 G; 184754 T; 247 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transgenic non-human animals (mice), useful as models for depression, for monitoring the efficacy of a drug against depression, and for screening antidepressants, drugs or genes for ameliorating or treating depression -
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wolfram Syndrome 1; WFS1; transgenic; wolframin; brain; depression; stress-induced neurochemical change; behavioural change; mouse; drug screening; antidepressant; gene; ds.
                                                                       3,
                                    DB 25; Length 659158;
                                                                       50; Indels
                                Score 82; DB 25;
Pred. No. 1.3e-11;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wild-type mouse Wolfram Syndrome 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Page 60-63; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA97708 standard; DNA; 10917 BP
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                               3.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                   Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                      439241 ACATGTGG 439234
                                                                                                                                                                                                                                                                                                                     378 ACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberds SL, Huff RM;
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-089969/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-2002
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                                    Query Match
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10457
                                                                                                                                       10340 TGCGAGGACAGAGGTTCTCAACCTGTGGGGCACAACCCCTTTGGGG--TTTGAATGACTT 10397
                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a viral infection gene. The present invention describes nucleic acid sequences isolated from rat. The sequences of the invention comprise 70 viral infection (VI) genes and 8 tumour suppressor (TS) genes. Propagating cell cultures in the absence of the serum protein (SP) allows selective elimination of cells persistently infected with a virus from the cell culture. Inhibitors of the SP can be used for reducing or inhibiting a viral infection. Inhibitors of the TS gene products can be used to suppress a malignant phenotype (MP). The methods and inhibitors can be used with viruses such as HIV, influenza, hepatitis virus or animal retroviruses such as simian immunodeficiency virus, avian immunodeficiency virus, bowine immunodeficiency virus, feline immunodeficiency virus, equine infectious
                                                                           10398 TICACAGGGTIGCTIGCCAAAGACCATCAGAAACACAGGIATITACATICCAATICAT
                                                                                                                  257 TTTACAGGGGTCACATATCA---TCTATCCTATATGTCAGGTATTTACATTACGATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes involved in viral infection and tumour suppression - used to develop products for reducing or preventing viral infection or for suppressing tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral infection, tumour suppressor, cellular gene, rat, cancer, serum protein, inhibitor, malignant phenotype, HIV; influenza, hepatitis, retrovirus, immunodeficiency, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 82-83; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral infection gene SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubin DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0015334.
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                                                                                                                                                                                                                                     10518 CACATCATGAAG 10529
                                                                                                                                                                                                                                                                                                                                        AAV06155 standard; DNA; 892
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                374 CACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVA-:) UNIV VANDERBILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dubois RN, Organ EL,
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177 CTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGGCCTCGACCCCT 236
                                                                                                                                                                                                                                                                             179 TIGGGAGTGCGGTCAAATGACCCCTATCACAGGGGTCTCAAATGAGATATCCTGCATATCA 238
                                                                                                                                                                                                                                                                                                                                         237 TIGGG---GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATCCTATATGTCA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                  293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 AATATTTACATTATGATTCATAGTAGTACCAGAATTACAGTTATGAAGTTACA---AAAT 295
anemia virus, caprine arthritis encephalitis virus or visna virus. Because the identified genes are non-essential to cell survival, the treatment methods can be used in subjects without serious detrimental effects to the subjects.
                                                                                                                                                                                                          7; Gaps
                                                                                                                                                      Query Match 3.3%; Score 78; DB 18; Length 892; Best Local Similarity 70.5%; Pred. No. 5e-12; Matches 148; Conservative 0; Mismatches 55; Indels
                                                                                                                 Sequence 892 BP; 224 A; 206 C; 185 G; 229 T; 48 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 AATTTTATAGCTGAGAGTCACCACAACATG 325
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Search completed: November 17, 2003, 23:52:49 Job time: 628.73 secs

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Seguence 3,

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Best Local Similarity 69.2
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
 RESULT 1
US-08-920-422-17/c
                                                                                                                                                                                                                                                                                                                         US-08-920-422-17
311
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Sequence 183, App
Sequence 183, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 38, Appl
Sequence 7, Appli
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Sequence 208, App
Sequence 207, App
Sequence 207, App
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Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 107, App
Sequence 107, App
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Sequence 157, App
Sequence 3, Appli
Sequence 3, Appli
                                                 November 17, 2003, 23:31:50 ; Search time 137.266 Seconds (without alignments) 7582.209 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Appl
Sequence 75, Appl
                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence Sequence Sequence Sequence
                                                                                                  1 ggatcctttcatgtttaaca......caggtcggaggccaccatgg
                                                                                                                                                                                                                            Issued Patents_NA:*
.: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/Regi:*
.: /cgn2_6/ptodata/2/ina/Regi:*
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                        569978 seqs, 220691566 residues
                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                   nucleic search, using sw model
                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                      seq length: 0 seq length: 2000000000
                                                                                US-10-005-337A-1
2358
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Match Length DB
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29604
29604
6645
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10614
10614
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                                                                                 Title:
Perfect score:
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                                                                                                                                                                      Minimum DB
Maximum DB
                                   OM nucleic
                                                                                                  Sequence:
                                                                                                                                        Searched:
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                                                   Run on:
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118
22
22
22
24
25
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27
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15325 A-CCTTTTCACAAGGGTCACATCAGAGATCCTGCATATCCGATATTTATGTT 15267
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Appli
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   Sequence 3, Appli
Sequence 14, Appl
Sequence 3, Appli
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                                                                                                                                                            168,
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                                               Sequence 3, P
Sequence 1, Sequence 1, P
Sequence 1, P
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Sequence 75, Application US/09171209

Sequence 75, Application US/09171209

GENERAL INFORMATION:

APPLICANT: VANDERBILT UNIVERSITY

305 Kirkland Hall

Nashville, TN 37240

TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 88.6; DB 3;
69.2%; Pred. No. 3.9e-16;
iive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08920422A
Fatent No. 6255473
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vitek, Michael P.
APPLICANT: Roses, Allen D.
TITLE OF INVENTION: Presentlin-1
FILE REFERENCE: VITEKPRESENILIN
CURRENT FILLING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 48974
US-09-577-806-3

US-08-212-463-14

US-08-212-463-14

US-09-244-796-3

US-08-462-509B-1

PCT-US-95-05616-1

US-08-46-706-1

US-08-46-704-1

US-08-846-704-3

US-09-220-132-168

US-09-078-294-4

US-09-078-294-3

US-08-602-264A-1

US-08-602-264A-1

US-08-46-1018A-1

US-08-46-1018A-1

US-09-622-540A-1
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NAME/KEY: exon
LOCATION: 1982:
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US-09-218-207-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 TTGGG---GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATCTTATGTCA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TIGGGAGIGCGGICAAAIGACCCIAICACGGGGICICAAAIGAGAIAICCIGCAIAICA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AATATTTACATTATGATTCATAGTAGTACCAGAATTACAGTTATGAAGTTACA---AAAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 CTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                         COUNTRY 1931

ZIP: 30303-1811

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.3%; Score 78; DB 4; Length 892;
Best Local Similarity 70.5%; Pred. No. 6.9e-14;
Matches 148; Conservative 0; Mismatches 55; Indels
                                            ADDRESSEE: Needle & Rosenberg, P.C. SYREF: 127 Peachtree Street, Suite 1200 CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION DATE: CUNKNOWN

FILING DATE: CUNKNOWN

ATTORNEY/AGENT INFORMATION:
NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298

TELERORMUNICATION INFORMATION:
TELEPHONE: 404,688,0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 AATTTTATGATTGAAGGTCACCACAACATG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AATTITATAGCIGAGAGICACCACAACAIG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET. 18CPLCP
CURRENT FILING DATE: 1999-06-23
CURRENT APPLICATION NUMBER: 08/996,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-171-209-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 183, Application US/09338907
Patent No. 6265546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 404 688 9880 INFORMATION FOR SEQ ID NO: 75: SEQUENCE CHARACTERISTICS:
SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-338-907-183
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9570 acctarccrectrarcagaractracarrareaarreraacagcagcaaaarcacagrra 9629
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3.2%; Score 74.8; DB 3;
Best Local Similarity 80.0%; Pred. No. 6.5e-12;
Matches 88; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCORMATION:
APPLICANT: Cohen Daniel
APPLICANT: Cohen Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE COFINENTION: Protate cancer gene
TITLE REFERENCE: GENSET, 018CP1
CURRENT FILING DATE: 1999-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 578
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER PILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SEQ ID NO 183
; SEQ ID NO 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 183, Application US/09218207
Patent No. 6346381
                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: exon
LOCATION: 5259..5328
OTHER INFORMATION: exon2
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 12675..12791
OTHER INFORMATION: exon3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: exon
LOCATION: 14621..14710
OTHER INFORMATION: exon4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 21789..21950
OTHER INFORMATION: exon6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 23387..23510
OTHER INFORMATION: exon7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 25520..26016
; OTHER INFORMATION: exon8
US-09-338-907-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: exon5
                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19822..19912
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REGISTRATION NUMBER: 31,298

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7155 TGACCCTTTCACAGGGGTCACCTAAGACCATCAGAAACACAGATATTTGCTTTATGATT 7096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7095 CATGACAGAAGCAAAATTATAGTTGTGAAGTAGCAATGAAAATAATTTCACAGTTGGGGG 7036
                                                                                                                                                                                                                                                                                                                                                                                                                ---GAATCAAA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/08187453
Patent No. 5753431
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Regulatory Elements and Transcription Factors
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE FOLSE FOLSE
STREET: 3000 K Street, N.W.; Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                        Length 10614;
                                                                                                                                                                                                                                                                                                                                                                                                             195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGG
                                                                                                                                                                                                                                                                                                                Query Match 3.2%; Score 74.6; DB 1; I
Best Local Similarity 64.0%; Pred. No. 3.5e-12;
Matches 130; Conservative 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,453
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLIANCE DATE: 3-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/188
18748/175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7035 TCACACACATCAGGAAGGTAGA 7013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 CACCACACATGAGGCCGCCACA 393
                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                             TOPOLOGY: linear . . MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                     single
                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-187-453-35/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chiang, John
TITLE OF INVENTION: Cholesterol 7a-Hydroxylase Gene
TITLE OF INVENTION: Regulatory Elements and Methods for Using Them
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9630 CGCAATATCAACAAAATTTTATGGTTGAGGGTCACCATAACGTGAGG 9679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 TGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 37950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74.8; DB 4; Length 379
Pred. No. 6.5e-12;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0; Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
HILING DATE: 13-OCT-1993

***ASTRICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-135-511-35/c
, Sequence 35, Application US/08135511
; Patent No. 5558999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2%;
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NAME: SANDERCOCK, Colin G.
                                        PEATURE:
FEATURE:
NAME/KEY: exon
LOCATION: 5259..5328

^THER INFORMATION: exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.09
Matches 88; Conservative
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                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 14621..14710
OTHER INFORMATION: exon4
                                                                                                                                                                                                LOCATION: 12675..12791
OTHER INFORMATION: exon3
                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 19822..19912
OTHER INFORMATION: exon5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 21789..21950
OTHER INFORMATION: exon6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 23387..23510
OTHER INFORMATION: exon7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 25520..26016
OTHER INFORMATION: exon8
              TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-218-207-183
                                                                                                                                                                                                                                                                                                                                                              JAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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Query Match
3.1%; Score 73.4; DB 4;
Best Local Similarity 70.2%; Pred. No. 4.7e-12;
Matches 127; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/272,496
CURRENT FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/092782
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 TTGAAGGTCACCACAACATGAGG 385
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US-08-781-891-208/c
; Sequence 208, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 69.5%;
Matches 141; Conservative C
  TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4072;
TYPE: DNA;
ORGANISM: Mus musculus
US-09-272-496-7
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                                           ; TOPOLOGY:
US-08-882-164D-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7095 CATGACAGAAGCAAATTATAGTTGTGAAGTAGCAATGAAAATAATTTCACAGTTGGGGG 7036
                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 CGACCCTTTACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGAAGGT 370
                                                                                                                                                                                                                                                                                                                                                                195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGG----GAATCAAA
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        Query Match

3.2%; Score 74.6; DB 1; Length 10614;
Best Local Similarity 64.0%; Pred. No. 3.5e-12;
Matches 130; Conservative 0; Mismatches 69; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAO, 1BM PC compatible OPERATING SYSTEM:
MS-DOS.5.1
SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/82,164D
FILING DATE: JUNE 25, 1997
FILING DATE: JUNE 21, 1996
FILING DATE: JUNE 21, 1996
FILING DATE: Occober 1, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: JUNE 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HULL, JOHN C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKTN UMBER: 36,424
REJECHALOXION NUMBER: 36,424
REJECHALOXION NUMBER: 36,424
REJECHALOXION NUMBER: 36,424
REJECHALOXION NUMBER: 36,424
REJECHALOXION NUMBER: 36,4344
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Sequence 38, Application US/08882164D

Patent No. 6306624

Patent No. 6306624

Patent No. 6306626

APPLICANT: Petkovich, P. Martin, White, Jay A.,

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 43

CORRESSEDNIBRICE ADDRESS:

ADDRESSED BLAE, Commerce Court West

CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7035 TCACACACATCAGGAAGGTAGA 7013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 CACCACACATGAGGCCGCCACA 393
                 TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4164 base pairs
                                                                                                                                                                                            linear
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COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: M5L 1A9
                                                                                                                                                                                          TOPOLOGY:
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1252 AGAGCTTTTCAACCTGTGGGTCGTGACCCCTTCACGGAGCCAAACAACCTTTCAGAAGG 1311
                                                                                                                                                                                                                                                           326 ATTACAGGTATGAAATAGCAATGAA-ATAATTTTATGATGGAGGTCACCACAACATGAG 384
                                                     206 AGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCTTTACAGGG 265
                                                                                                                                                        266 GTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GACCGTAGAGCACAGGTTCTCAATCTGTGGGTCGCAACCCCTTT-GGGCATCCAAAAGCA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 TACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATG-AAATAATTTATGA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTTGGACCCCTTTGGGGGAATCAAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: DEGregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
     Gaps
  <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68.6; DB 3; 1
Pred. No. 1.4e-10;
0; Mismatches 49;
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5983 TTACATCACAATTCATAACGGTGGCAAAATTACAGTCAAGAAGTAGCAAAGGAAATAATG 5924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 TTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATATTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.9%; Score 68; DB 4; Length 16442;
66.2%; Pred. No. 5e-10;
ive 0; Mismatches 50; Indels
                        ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
CORRESPONDENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                             TILING TATION: «URKNOWN»

ATTORNEY/AGENT INFORMATION:
NAME: MCMSterer, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELEPHONNE: (206) 622-4900
TELEPHONNE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5923 rcarggrrggrccarcacacacacas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 208: US-09-618-166-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 TATGATTGAAGGTCACCACAACATGAGG 385
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FTI.ING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 207, Application US/08781891
Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16442 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.24
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SEED and
STREET: 6300 Columb
CITY: Seattle
STATE: Washington
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US-08-781-891-207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 TTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATGAAATGAAATAATTT 357
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Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
FITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.9%; Score 68; DB 3; Length 164
Best Local Similarity 66.2%; Pred. No. 5e-10;
Matches 98; Conservative 0; Mismatches 50; Indels
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ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle STATE: Washington
APPLICANT: Yu, Chang-En
APPLICANT: Obhima, Junko
APPLICANT: Cabhima, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5923 rcargerrecreccárcacacacacases 5896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 209
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STRANDEDNESS: single
                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                  Seattle
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                                                                                                                                                                                                                                                          STATE: WA
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Gaps

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262 AGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAG 321
                                                   0; Gaps
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US-08-380-403A-4/c
Sequence 4, Application US/08380403A
Sequence 4, Application US/08380403A
Sequence 4, Application US/08380403A
Setent No. 5831024
GENERAL INFORMATION:
APPLICANT: MANATO, Magahiro
APPLICANT: HATTORI, Masakazu
APPLICANT: HATTORI, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
Score 65.6; DB 4; Length 29604;
Pred. No. 4e-09;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                              18808 CAAAATTACAGTTATGAAGTACCAATGAAATCATTTTATGGTTG 18851
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/380,403A
FLING DATE: 30-04N-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,909
FLING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6-279712
FLING DATE: 20-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6-279712
FLING DATE: 30-0AT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 53466/128/AAOK
TELECOMMUNICATION INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 53466/128/AAOK
TELEBEHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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      2.8%;
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  Query Match
Best Local Similarity 76.9%
Matches 80; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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TTY: Washington
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LOCATION:
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Pred. No. 4e-09;
0; Mismatches 24; Indels 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CIASSIFICATION: CUNKNOWN>
ATORNEY/AGENT INFORMATION:
NAME: MCMSGLETS, DAVIG D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET WUMBER: 240052.419C1
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 CAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue; Suite 6300
                    NAME: No. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
SEQUENCE CHARACTERISTICS:
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US-09-618-166-207
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 207, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
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                                                                                                                                                                                                       LENGTH: 29604 base pairs
TYPE: nucleic acid
TYRE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-207
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fu, Ying-Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 76.9
Matches 80; Conservative
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US-09-618-166-207
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                                                                                                                                               Gaps
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HATTORI, Masakazu
HIROSHI, Kubota
MASATSUGU, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 7
..4903, 5017..5117, 5200..5255, 5447..5525, 5598
..5741)
                                                                                                  Length 6645;
                                                                                                2.8%; Score 65; DB 2; Length 664
72.3%; Pred. No. 2.5e-09;
tive 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,810D
FILING DATE: 17-Jul-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/128/AAOK
                                                                                                                                                                                                                                                                                                                                                                       351 ATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                   434 AATAATTTTGA-TCAGGGTCACCACACCATGTGG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-7AN-1995
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-0CT-1994
APPLICATION NUMBER: UP 6-279712
FILING DATE: 20-0CT-1994
APPLICATION NUMBER: UP 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/380,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08895810D Patent No. 6406886
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 6645 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                             Query Match
Best Local Similarity 72.33
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C
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                                ; LOCATION:
US-08-895-628-4
         LOCATION:
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                                                                                                    291 CAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAA 350
                                                                                                                                                                                           233 CCCTTTGGGGGAATCAAACGACCCTTTACAGGGGTCACAT--ATCATCTATATGT
                                Gaps
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..2618, 2890..3164, 4291..4509, 4598..4709, 4795
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08895628
Patent No. 5998585
GENERAL INFORMATION:
APPLICANT: MINATO, Nagahiro
APPLICANT: HIROSHI, Rubota
APPLICANT: HIROSHI, Rubota
APPLICANT: MASATSUGU, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
         Pred. No. 2.5e-09;
0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,628
                                                                                                                                                                                                                                                        351 ATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                   434 AATAATTTTGA-TCAGGGTCACCACCATGTGG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/380,403
FILING DATE: 30-JAN-1995
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-279712
FILING DATE: 20-0CT-1994
APPLICATION NUMBER: JF 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROID C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/128/AAOK
TELECOMMUNICATION INFORMATION:
NAME: WEGNER, HAROID C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/128/AAOK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
       Best Local Similarity 72.3%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6645 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DECOLUTE (202) 0.2 TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS:
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US-08-895-628-4/C
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NAME/KEY:
LOCATION:
LOCATION:
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233 CCCTTTGGGGGAATCAAACGACCCTTTACAGGGGTCACAT--ATCATCTATCTATATGT 290
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; NAME/KEY: CDS
; LOCATION: join(904..1015, 1356..1459, 1726..1883, 2009
; .2618, 2890..3164, 4221..4509, 4598..4709, 4795..4903,
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-895-810D-4
                                                                                                                                               Query Match 2.8%; Score 65; DB 4; Length 6645; Best Local Similarity 72.3%; Pred. No. 2.5e-09; Matches 112; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                            351 ATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
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Search completed: November 18, 2003, 07:06:16 Job time : 147.266 secs

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63.2
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60.4
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                                                                                                     November 17, 2003, 23:33:10 ; Search time 1128.46 Seconds (without alignments) 6829.176 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2 6/prodata/1/pubpna/US07 PUBCOMB.seq:*
2: /cgn2 6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2 6/prodata/1/pubpna/DS06 NEW_PUB.seq:*
4: /cgn2 6/prodata/1/pubpna/US06 NEW_PUB.seq:*
5: /cgn2 6/prodata/1/pubpna/US06 NEW_PUB.seq:*
6: /cgn2 6/prodata/1/pubpna/US08 NEW_PUB.seq:*
7: /cgn2 6/prodata/1/pubpna/US08 NEW_PUB.seq:*
8: /cgn2 6/prodata/1/pubpna/US08 NEW_PUB.seq:*
9: /cgn2 6/prodata/1/pubpna/US08 NEW_PUB.seq:*
9: /cgn2 6/prodata/1/pubpna/US09 NEW_PUB.seq:*
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11: /cgn2 6/prodata/1/pubpna/US09 NEW_PUB.seq:*
13: /cgn2 6/prodata/1/pubpna/US09 NEW_PUB.seq:*
14: /cgn2 6/prodata/1/pubpna/US10A PUBCOMB.seq:*
15: /cgn2 6/prodata/1/pubpna/US10A PUBCOMB.seq:*
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17: /cgn2 6/prodata/1/pubpna/US10A PUB.seq:*
17: /cgn2 6/prodata/1/pubpna/US10A PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-175-523-80
US-09-771-208-20
US-10-175-523-97
US-10-002-631C-156
US-10-175-523-62
US-10-175-523-62
US-10-26-188-3
US-10-26-188-3
US-10-026-188-3
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US-09-901-484A-183
US-09-853-526-183
US-10-025-966A-24
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Listing first 45 summaries
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2358
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Match
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88.8
88.8
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1261 TAAATATTATATTTTCACATTTTAATATCTTAGCGATGACAAGCAGAAACAAGTATT	Qy 1441 ACGCACATTTTCTCGGGCTCTCTTAAGCTTTTCCCACAGCATTGGGAAACTTTACTGAC 1		Qy         1621 GCACTAATTATGGCCAGTGACACCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTT 1	16	1741   AGASTICCAACAGATGAGACAAGTGGGCACCCCAGCCTCTTCCTTC	Oy 1861 GTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGAT 1	1921 ACGTTAGTCATATGAGAGCTGACAAAAAAAAAAAAGGCAGCGATGTGGTGCAATATTA 	1981 ACAGGAACTGTCCCCTGGCTTCCCGATACGTGGCATGACTCGCATTGCTGAACCGTTGTG	Qy 2041 GTCACTGCCAAAGGAATGACCCTCTCACATTCTTCTTCTTCATTCGCTACGCCGCGCCAG 2	Qy 2101 CTTGTCATCTCCTTTGGGCTTCCCAGACACTAAGTCTGGAATGAAATTCACCTGCCT 2  Db 2101 CTTGTCATCTCCCTTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCT 2	Qy         2161         CTGAATTGGCCACTGGTGGGGGCAGGGTGTGACTTGGCTTCCCAGGTGGAGATTATC         2	Qy         2221         TCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAG         2	Qy 2281 GGGTTCATCCACAAGAGAAAACATAGACTCGAGGTCTAGGGGAGCTTGCATGCCTGCA 2
181 TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGG 240  181 TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGG 240  241 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA 300  241 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA 300  301 CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATATTTAT 360  301 CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATATTTAT 360  301 CATTACGATTCGTAACACACACACACATACAATACAATA	61 GATTGAAGGTCACCACAACATGAGGCCGCCACAGTTCTAGAGAAAATCACCTGGGTG 4	421 GGGAAAGGTTTGGGAAAGCCTTTCTGTCATTCTTCAAAGTGATGTGTTCACA 480 421 GGGAAAGGTTTGGGAAAGCCTTTCTGTCATTCTTCAAAGTGATGTTCTCACA 480 421 GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCAAAGTGGATGTTTCACA 480 481 GAAAGCCTTTCAGCTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTATGTA	41 CAGGTCTGCTTCTTATGGGTGGAGCCAAGACGCATCGTGGGTGG	ATCT ATCT ATCT	1 CTGTGAATCGAGATCCTTGGCTTGGATTAGGGAGGCACAAAATACTCAGAGATTC 72  1 AAGACTGCTCAGCACCCCAGAGTCCTTCCTCAAAGGAAGG	TAGGARACCACAGAGGACATACGAAAAGGAAAAGGAAAAGGAAAAGAAAG	41 CTTGTCACTTCAAGAGGTCAAAGAAATAGTGTTAACCATGAAAACGAGAAGACCAACAG 90 CTGTCACTTCAAGAGGTCAAAAAAAAAAAAAAAAAAAAA	901 TTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAGAGAG	961 CACGAAGGACAAGGTATTAGTGTTTGTGGGGGAATGTCTTGTACTGAAGATTCT 1020 	21 AGAAACACAATTIGCTGGTTGAACAGCTGAAGTGGGGTGGG	1 TGGAAGGGTGAAGAGAGAGAGATATATGATGGCCAGCATAACAAACA	1 CCCTAATTAACACTTCCCTCTTCTACTAACACCCTCAGCATACTTACATAAAAA 12  1 CCCTAATTAACACTTCCCTCTTCTACTGACACCCCCTTCACTCCTCTCTTCATAAAAA 12  1	1 CCCIAALIAACATITCCTGCTTTTTTTTTTTTTTTTTTTTTTTTTTT

us-10-005-337a-1.rnpb

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APPLICANT: BJOCANGIN, USLINEY
APPLICANT: BJOCANGIN, USLINEY
APPLICANT: HOOK, Derek
APPLICANT: Klinczak, Leszek
APPLICANT: Klinczak, Leszek
APPLICANT: Rijenczak, Leszek
APPLICANT: Rijenczak, Leszek
APPLICANT: Rajan, Prithi
FILE REFERENCE: 3238/1J795-US3
CURRENT FILING DATE: 2002-06-18
FILE REFERENCE: 3238/1J795-US3
CURRENT APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                   GTGTGGAGGGCTCCACAGGCCCAGTTCCAGGGGTTCATCCACAAGAGAAAAAAATAG 2309
                                                                                                                                                                                                                   1998 GTGTGGAGGGCCCAGCAGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAAAAA 2056
                                                                                TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56571 TCATAGAGGTCACATATCTGATATCTTGCATATCACATATTTACATTACGATTCATAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56512 TCTATAGCAGTGGTTCTCAACCAGTGGCTCATAACCCCTATGGTGG-CTGAATGACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 TTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 90650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 80, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-175-523-80
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                                                                                                                                           Sequence 2, Application US/1000337A
Publication No. US20030039984A1
Publication No. US20030039984A1
GANERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: BRANELLEC, Didier
APPLICANT: GHEN, Kenneth R.
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE OF INVENTION: THEM AND USES THEREOF
TILE OF INVENTION: THEM AND USES THEREOF
THE REPERENCE: 03806.0530-00000
CURRENT APPLICATION NUMBER: US/10/005,337A
CURRENT APPLICATION NUMBER: US 60/251,582
RIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 2074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCCAGAC 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1585 C---CTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAGATATTACTGGGGGTGTGATA 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATCTCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTC 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1525 CCAGATCCCTTCCCCTCAGGCTGTTTACCCAGGGAATAGGATGTCCTGGGACAAGTTTCC 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCCAACTGGAGGCTGATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATG 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1898 CACAGTGC--TTGCATTTTCTTGATACGTTAGTCATATGAGAGCTGACAAAGAAGAAAA 1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGATTCGCATACGCCGCGG-----CCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGAC 2130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1406 GCATTACTGAATGCTTTCAATGTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1598 TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1349 TradaAcaccicaracarcracicara---arcccacacacarcaraaaagaaaacr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1466 TTTAGC-CCAGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%; Score 367.8; DB 14; Length 2074; 76.4%; Pred. No. 3.4e-101; ive 0; Mismatches 162; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.4
Matches 597; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-337A-2
                                                                                                RESULT 2
US-10-005-337A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1718
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35071 TCTAATACAATGATTCTTAATCTGTGGGGAGTGGCCTCTTTAGGAGGTTCAAAGGACCTT 35130
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APPLICANT: Hook, Derek
APPLICANT: Klimczak, Leszek
APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Laeng, Pascal
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1/1795-US3
CURRENT APPLICATION NUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 TTACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACA 317
-- TGATTGAAGGTCACCACAAC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 GTAGCAAAATTACAGGTATGAAATAGCAAT-GAAATAATTTTATGATTGAAGGTCACCAC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCCT
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68.8%; Pred. No. 6e-13;
tive 0; Mismatches 58;
  324 AAATTACAGGTATGAAATAGCAATGAAATAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2004-06-189
FRIOR APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
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PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                               Sequence 97, Application US/10175523 Publication No. US20030096264A1 GENERAL INFORMATION: APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09771208
Patent No. US20020155564A1
GENERAL INFORMATION:
APPLICANT: MEDRANO, JUAN
APPLICANT: BRADFORD, ERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus musculus domesticus
US-10-175-523-97
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Matches 130; Conservative
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                                                                                                        380 ATGAGG 385
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US-09-771-208-20/c
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                                                                                                                                                     APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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3.8%; Score 88.8; DB 10;
Best Local Similarity 74.7%; Pred. No. 8.5e-14;
Matches 139; Conservative 0; Mismatches 42;
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LOCATION: (123459)...(12478)
CUTER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (602466)...(602485)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (546598)...(547017)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (494715)...(494814)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (130586)...(391005)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (1346860)...(346823)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (316860)...(346823)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (210774)...(317193)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (280353)...(280373)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (217829)...(271848)
OTHER INFORMATION: nis unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (271829)...(271848)
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LOCATION: (183572)..(183891)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified a,
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CTHER INFORMATION: n is a, c, g, or
US-09-771-208-20
                                               Sequence 20, Application US/09771208 Patent No. US20020155564A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mus musculus
                                                                                                     GENERAL INFORMATION:
APPLICANT: MEDRANO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 659158
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Publication No. US20030167488A1

GENERAL INFORMATION:

APPLICANT: Roberds, Steven L

APPLICANT: Huff, Rita M

TITLE OF INVENTION: MICE HETRROZYGOUS FOR WFS1 GENE AS MOUSE MODELS FOR

TITLE OF INVENTION: DEPRESSION

TITLE OF INVENTION: DEPRESSION

FILE REPERBNCE: 28341/6284.N

CURRENT APPLICATION NUMBER: US/10/195,963

CURRENT APPLICATION NUMBER: US/09/871,107

PRIOR APPLICATION NUMBER: US/09/871,107

PRIOR SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 10917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 CAACACCCTTTGGGCGTCCTATATCCGATATCCTGCATATTTTACATGACGATT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                    Sequence 156, Application US/10002631C

Publication No. US20030157486A1

GENERAL INFORMATION:

APPLICANT: Graff, Jonathon M.

APPLICANT: Muenster, Matthew

TITLE OF INVENTION: METHODS TO 10002,631C

FILE REFERENCE: A34943 090495.0743

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: 60/300,309

PRIOR FILING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 324

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 156

LENGTH: 889
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%; Pred. No. 1.7e-12;
0; Mismatches 51;
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i OTHER INFORMATION: n = A, C, G or T
US-10-002-631C-156
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; LOCATION:
; OTHER INFORMATION: m=a or c;
US-10-195-963-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 74.81
Matches 101; Conservative
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Best Local Similarity 70.81
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
                                                                      US-10-002-631C-156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439300 GTAGCAAAATCACAGTTATGAGGTAACAATGAATGATTTTATGGTTG-GGGTCACCGCA 439242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439358 TT--CTGCGTAGCATATCAGACATCCTGCATATCAGATATTTCCATTATGACACATAATG 439301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 TTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGCAAAATTACAGGTATGAAATAGCAATGAAATATTTTATGATTGAAGGTCACCACA 377
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APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 4017-923710US
CURRENT APPLICATION NUMBER: US 08/99171,208
FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR APPLICATION NUMBER: US 08/999,477
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (183872)..(183891)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OCATION: (123459) .(123478)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                EX: misc_feature
ON: (546998)..(547017)
INFORMATION: n is unidentified a,
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ION: (494715)..(494814)
INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEY: misc feature
ION: (390986)..(391005)
I INFORMATION: n is unidentified a,
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TION: (346B60)..(346823)
R INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: misc feature
OCATION: (280353)..(280373)
THER INFORMATION: n is unidentified a,
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LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified
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; OTHER:INFORMATION: n is a, c, g, or
US-09-771-208-20
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                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGAGG 385
                                                                                                                                                                                            SEQ ID NO 20
LENGTH: 659158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
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APPLICANT: BLOCKING.
APPLICANT: BLOCKING.
APPLICANT: Klinczak, Leszek
APPLICANT: Klinczak, Leszek
APPLICANT: Klinczak, Leszek
APPLICANT: Leang, Pascal
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANTON: MULTI-PRAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1J795-US3
CURRENT PAPLICANTON NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                        10458 GACAGTAGTAAAATTACAGTTATGCAGTAGCAATGAAAATAATTTTATGGTTGGGGTGAC 10517
                                                            10340 receaddacadactricidaactrigaddacadaacccirrigddd-rrrgaardacrr 10397
                                                                                                                                                                                        10398 TICACAGGGTTGCTTGCCAAAGACCATCAGAAACACAGGTATTTACATTCCAATTCAT 10457
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                                                                                                                                                                                                                                                           323 AAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAACATG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 GGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGC 322
                                                                                                                               TTTACAGGGGTCACATATCA---TCTATCCTATATGTCAGGTATTTACATTACGATTCGT
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Pred. No. 6.2e-11;
0; Mismatches 28; Indels
   TTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 62, Application US/10175523
Publication No. US20030096264A1
GENERAL INFORMATION:
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1 Similarity 77.2%;
95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           CACAACATGAGG 385
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Best Local Similarity
Matches 95; Conserval
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LENGTH: 185548
197
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RESULT 10 US-10-228-794-75

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 ingegagnecegicaangacecharcacaeeerercaangaganateerecaratea 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATTAGAAATGAAAT .352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 CTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCT
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                                                                                                       305 Kirkland Hall
Nashville, TN 37240
TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78; DB 14;
Pred. No. 1.5e-12;
0; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0061/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
APPLICATION NUMBER: PCT/US97/06067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 AATTTTATGATTGAAGGTCACCACAACATG 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 27-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-228-794-75
                                                   GENERAL INFORMATION:
APPLICANT: VANDERBILT UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          STATE: Georgia
COUNTRY: USA
ZIP: 3033-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 75, Application US/10228794
Publication No. US20030027198A1
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Publication No. US20020164645A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 404 688 9880 INFORMATION FOR SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.3%;
Best Local Similarity 70.5%;
Matches 148; Conservative
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-026-188-3/c
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4978 ACTCTAAGCCTGTGGTTCTCAACCCATGAGTCATGACCCTTTGGGATTGTCCAATGACCC 4919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 CTTT---ACAGGGGTCACATATCATCTATATGTCAGGTATTACATTACGATTCG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 TAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCA 372
                                                                                                     269 ACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 ATTOTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
US-09-917-800A-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%; Score 75.6; DB 10; Length 5990; 66.7%; Pred. No. 3.3e-11; ive 0; Mismatches 59; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Castle, Arthur APPLICANT: Castle, Arthur APPLICANT: Elashoff, Michael APPLICANT: Elashoff, Michael APPLICANT: Elashoff, Michael APPLICANT: Elashoff, Michael APPLICANT: Gene Logic, Inc.: TITLE OF INVENTION: Molecular Toxicology Modeling FILE OF INVENTION: MOBER: US/09/917,800A CURRENT APPLICATION NUMBER: US 60/222,040 PRIOR APPLICATION NUMBER: US 60/222,040 PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR APPLICATION NUMBER: US 60/290,029 PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: US 60/290,645 PRIOR APPLICATION NUMBER: US 60/290,455 PRIOR APPLICATION NUMBER: US 60/292,336 PRIOR FILING DATE: 2001-05-15 PRIOR APPLICATION NUMBER: US 60/292,798 PRIOR PRIOR DATE: 2001-06-06 PRIOR PRIOR DATE: 2001-06-06 PRIOR APPLICATION NUMBER: US 60/295,798 PRIOR FILING DATE: 2001-06-19 PRIOR APPLICATION NUMBER: US 60/296,884 PRIOR APPLICATION NUMBER: US 60/296,884 PRIOR APPLICATION NUMBER: US 60/296,884 PRIOR APPLICATION NUMBER: US 60/296,884 PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PILING DATE: 2001-06-19 PRIOR PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 477, Application US/09917800A Patent No. US20020119462A1
                                                                                                                                                                                                                                   329 ACAGGTATGAAATAGCA 345
                                                                                                                                                                                                                                                                                     319 ACAGTTATGAAGTAGCA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%
Query Match
Best Local Similarity 66.7%
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-917-800A-477/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 91, Application US/09728445

Sequence 91, Application US/09728445

Patent No. US20020102543A1

GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: No. US20020102543A1e1
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT PILING DATE: 1999-12-01

NUMBER OF SEQ ID NOS: 891

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 91

LENGTH: 335

LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 CITICAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.3%; Score 76.8; DB 13; Length 249487; 70.2%; Pred. No. 2e-10; ive 0; Mismatches 57; Indels 5;
                       APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
TITLE OF INVENTION: ON Chamel
FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US,10/026,188
CURRENT FILING DATE: 2000-12-21
FRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 249487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.2%; Score 75.8; DB 10; Length 335; Best Local Similarity 81.8%; Pred. No. 3.6e-12; Matches 112; Conservative 0; Mismatches 22; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: mouse genomic region containing ltrpc5
US-10-026-188-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238423 rerecrirecacarcaccacacarcades
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)....(335)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3
Best Local Similarity 70.2
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-728-445-91
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210 GTTCTCAACCTGGGGGCCTCGACCCTTTGGGGGAATCAAACGACCCTTT-ACAGGGGTC 268

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Sequence 133, Application US/09901484A
; Patenne 10.0520020119460A1
; GENERAL INFORMATION:
    APPLICANT: Cohen, Daniel
    APPLICANT: Chumakov, Ilya
    APPLICANT: Chumakov, Ilya
    APPLICANT: Chumakov, Ilya
    APPLICANT: Chumakov, Ilya
    APPLICANT: Chumakov, Ilya
    APPLICANT: Chumakov, Ilya
    APPLICANT: Chumakov, Ilya
    APPLICANT: Bougueleret, Lydie
    TILE OF INVENITION: Prostate Cancer Gene
    TILE REFERENCE: GEN-TILIXCIDIZ
    CURRENT FILING DATE: 1907-07-09
    PRIOR APPLICATION NUMBER: US 08/996,306
    PRIOR APPLICATION NUMBER: US 09/218,207
    PRIOR FILING DATE: 1998-09-09
    PRIOR FILING DATE: 1998-09-09
    PRIOR FILING DATE: 1999-06-23
    PRIOR FILING DATE: 1999-06-23
    PRIOR FILING DATE: 1999-06-23
    PRIOR FILING DATE: 1999-06-23
    PRIOR FILING DATE: 2001-05-11
    NUMBER OF SEQ ID NOS: 578
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 183
    LENGTH: 37950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (616)...(616)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc_feature
LOCATION: (1552)...(1552)
OTHER INFORMATION: n = a, c, g, or t.
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LOCATION: (2821).. (2824)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc_feature
LOCATION: (2826).. (2826)
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OTHER INFORMATION: n = a, c, g, or NAME/KEY: misc feature
OTHER INFORMATION: n = a, c, g, or NAME/KEY: misc feature
LOCATION: (2835)...(2835)
OTHER INFORMATION: n = a, c, g, or NAME/KEY: misc feature
LOCATION: (5259)...(5328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WAME/KEY: misc feature
LOCATION: (2809)..(2809)
THER INFORMATION: n = a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (282\overline{6})...(2826)

OTHER INFORMATION: n = a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (6247). (6247)
OTHER INFORMATION: n = a, c.
NAME/KEY: misc feature
LOCATION: (8667). (8667)
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OCATION: (5259)..(5328)
THER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (8671)..(8679)
OTHER INFORMATION: n = a,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
4798 CTACAA 4793
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9570 ACCTATCCTGCTTATCAGATAGTTACATTATGAATTGTAACAGCAGCAAAATCACAGTTA 9629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 TGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 37950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74.8; DB 10;
Pred. No. 2.2e-10;
0; Mismatches 22;
CCATION: (8687)

OTHER INFORMATION: n = a, c, g, or t. NAME/KEY: misc feature
LCCATION: (8689)

OTHER INFORMATION: n = a, c, g, or t. NAME/KEY: misc feature
LCCATION: (8698)

OTHER INFORMATION: n = a, c, g, or t. NAME/KEY: misc feature
LCCATION: (8698)

OTHER INFORMATION: n = a, c, g, or t. NAME/KEY: misc feature
LCCATION: (9662)

OTHER INFORMATION: n = a, c, g, or t. NAME/KEY: misc feature
LCCATION: (12298)

OTHER INFORMATION: n = a, c, g, or t. NAME/KEY: misc feature
LCCATION: (12298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCCATION: (17639)...(17639)

OTHER INFORMATION: n = a, c, g, or t.

NAME/KEY: misc feature
LCCATION: (17707)...(17707)

OTHER INFORMATION: n = a, c, g, or t.

NAME/KEY: misc feature
LCCATION: (17867)...(17867)

OTHER INFORMATION: n = a, c, g, or t.
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; LOCATION: (37931) .. (37931)
; OTHER INFORMATION: n = a, c, g, or t.
US-09-901-4844-183
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Patent No. US20020165345A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (17578)..(17578)
OTHER INFORMATION: n = a, c,
NAME/KEY: misc_feature
LOCATION: (17639)..(17639)
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (12675)..(12791)
OTHER INFORMATION: exon 3
NAME/KEY: misc_feature
LOCATION: (14621)..(14710)
OTHER INFORMATION: exon 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (1982).. (19912) OTHER INFORMATION: exon 5 NAME/KEY: misc feature LOCATION: (21789).. (21950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon 6
NAME/KEY: misc feature
LOCATION: (23387)..(23510)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (25520)..(26016)
OTHER INFORMATION: exon 8
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9630 CGCAATATCAACAAAATAATTTTATGGTTGAGGGTCACCATAACGTGAGG 9679

Search completed: November 18, 2003, 07:42:01 Job time : 1143.46 secs

(USPTO) ANALB 3DA9 SIHT

us-10-005-337a-1.rst

8.1 478 12 BI293043 7.8 434 10 BF543101 7.3 488 9 AW252440	7.3 511 9 AW251306 7.1 370 9 AI710529 5.6 735 9 AU139209	5.1 509 10 BE627514 4.9 538 28 AZ804735 4.9 522 28 AQ480395 4.9 518 28 AZ114168	596 28 AZ290439 623 10 BB470796 577 28 AZ334079 556 28 AZ373614	4.6 589 28 BH360537 4.5 819 28 BZ110003 4.5 319 28 AZ600690	4.5 45-5 11 AKUSA932 4.5 3534 11 AKU38950 4.4 310 28 AZ939809	4.4 585 14 CA802248 4.4 834 28 BZ18556 4.4 519 28 AZ488841 4.4 640 29 BZ233325	103         4.4         574         28         A2563281         A2563281         A2563281         A2563281         A2563281         RPCI-23-2           102.6         4.4         810         29         B2564838         B2264838         CH230-315           102         4.3         364         28         A2348698         AZ348698         1M0085D24	4.3 7/4 28 BZ189530 4.3 676 28 AZ496223 4.3 594 28 AZ389177 4.3 477 28 AZ778894	4.3 596 28 AZ856151 4.3 407 13 BY549634 4.3 600 12 BG803092	4.3 591 28 AZ445982 4.3 787 28 BZ128535 4.3 803 29 BZ234545	4.3 2591 11 AK036783 4.2 1085 29 BZ223957 4.2 473 28 AZ060257	ALIGNMENTS	1 BH043261 ION RPCI-24-330A6.TJ RPCI-24 Mus musculus genomic clone RPCI-24-330A6, ON BH043261 BH43261.1 GI:14825212	Mus musculus (house mouse)  Mus musculus  Bukaryota, Matazoa, Chordata, Craniata, Vertebrata, Buteleost  Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,  (bases 1 to 600)		Other GSSs: RPCI-24-330A6.TV Contact: Shaying Zhao Department of Bukaryotic Genomics The Institute for Genomic Research	AC library
			C 15 C 17 18			C 25 C 26 28	0 29 0 31 0 32	Ω Δ Η Ε Ε Ε Δ Η Ε Ε Ε	337 38 39	0 4 4 4 4 2 4 2 4 2 4 2 4 2 4 2 4 2 4 2	44 44 44 5		RESULT 1 BH043261 LOCUS DEFINITION ACCESSION VERSION	SOURCE SOURCE ORGANISM REFERENCE	TITLE	COMMENT	
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	, using sw model	Run on: November 17, 2003, 23:31:10 ; Search time 4918.71 Seconds (without alignments) 11651.427 Million cell updates/sec	Title: Perfect score: 2358 Sequence: 1 ggatcctttcatgtttaacacaggtcggaggccaccatgg 2358	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	22781392 segs, 12152238056 residues	Total number of hits satisfying chosen parameters: 45562784 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	H .	3: em_estin:* 4: em_estmu:* 5: em_estcov:*	็ ย ย ย			16: em_eston:* 17: em_gss_inv:* 18: em_gss_inv:* 19: em_gss_pln:* 20: em_gss_man:* 22: em_gss_man:* 23: em_gss_man:*	25: em_gss_rod:* 26: em_gss_rod:* 27: em_gss_vri:* 28: gb_gss2:* 29: gb_gss2:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	\$ Result Query No. Score Match Length DB ID	1 585 24.8 600 28 BH043261 BH043261 RPCI-24-3 2 505.4 21.4 586 28 AZ295534 AZ295534 RPCI-22-1 3 306.8 13.0 371 13 BY091041 BY091041 BY091041 4 269.6 11.4 353 13 BY079997

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/clone lib="RPCI-23"
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
BCORI; Site_2: EcoRI; Female CS7BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                         Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 105 row: P column: 3
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 586)
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    RPCI-23-105P3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-105P3
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                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Contact: Shaying Zhao
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Pax: 301 838 0200
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-105P3"
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Mus musculus
                             genomic survey sequence.
                                                                  AZ295534.1 GI:9537319 GSS.
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Matches 531; Conservative
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                                                                                                                                                                                                                                                                                                              /gex="Male" // (Cell type="Spleen/Brain" // (Cell type="Spleen/Brain" // (Clone lib="RPCI-24" // (Clone library produced by Pieter de Jong. The RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using Mbol partially digested male C57BL/63
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library availability, please contact Pieter de Jong (pdeJong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://ww.chori.org/bacpac/orderingframe.htm). BAC epage: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 330 row: A column: 6 Seq primer: SP6 Class: BAC ends.
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Computerional Anialysis of Full-Lenguin Mouse Curhas Computer with Human Genome Sequences Mamw. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated Sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Flusher details
                      T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, M., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
            Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane
                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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|clone="K630084E21"
|tissue_type="heart"
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/strain="C57BL/6J"
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Sokazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schonbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Osato, N.; Blake, J.A.; Bradt, D.; Brusic, V.; Chochia, C.; Crobani, J.E.; Cousins, S.; Dalla, E.; Dragani, T.A.; Fletcher, C.; Forrest, A.; Frazer, R.S.; Gasserelland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I.J.; Jarvis, E.D.; Kanal, A.; Kawaji, H.; Kawasawa, Y.; Lenhard, B.; Lyons, M.; Kanal, A.; Kawaji, H.; Kawasawa, Y.; Lenhard, B.; Lyons, R.; Maglott, D.R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W.J.; Pertea, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Oi, D.; Ramachandran, S.; Ravasi, T.; Reed, J.C.; Reed, D.J.; Reid, J.; Raid, S.; Ravasi, T.; Reed, J.C.; Reed, D.J.; Reid, J.; Raid, M.; Shimada, K.; Sultana, R.; Aschala, Y.; Carmle, C.; Wang, Y.; Watanabab, Y.; Walls, C.; Walming, L.; Wahlsew-Boris, A.; Yang, I.; Yang, L.; Yang, I.; Yang, L.; Yang, I.; Wahlsew-Boris, A.; Yang, I.; Yang, L.; Yang, I.; Wahlsew-Boris, A.; Yang, I.; Yang, I.; Yang, I.; Yang, I.; Wahlsew-Boris, A.; Yang, I.; Yang, I.; Yang, I.; Wahlsew-Boris, A.; Kawai, D.; Alakawa, T.; Ronno, H.; Nakawura, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Arahawa, T.; Ronno, H.; Nakawa, T.; Rohi, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Satou, M.; Materston, R.; Lich, M.; Satou, M.; Materston, R.; Satani, D.;
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BY091041 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630084E21 5', mRNA sequence.
                                                                                                    2124
                                                                                                                                                                                                                        CCAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCA 2184
                                                                                                                                                                                                                                                                                                                                               GGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACG 2244
CCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCA 418
                                                                                                                                                                                                                                                                                                                                                                                                                478
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                         TCACATITICITICOTGATICGCATACGCCGCGCCAGCTIGICATCTCCCCTCTTGGGCTTC
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URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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PUBMED
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BY079997 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630022E19 5', mRNA sequence.
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                                                                                                                                                                                                                           2068 CATTICITCCIGATICGCATACGCCGCGCCCAGCTIGICAICTCCCTCTIGGGCTICCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAAAT
                                                         Gaps
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Score 306.8; DB 13; Length 371;
Pred. No. 1.8e-72;
); Mismatches 2; Indels 0;
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BI293043 1near EST 19-JUL-2001
UI-R-DKO-cdj-f-07-0-UI.sl UI-R-DKO Rattus norvegicus CDNA clone
UI-R-DKO-cdj-f-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 GCTGGTGTGGAGGGGCTCCACAGGCCAGTT-CAGGGGTTCATCCACAAGAGAGAAAAAC 298
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                                      /dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CACATTICTICCIGATICGNATACGCCGCGGNCAGCTIGICAICTCCCTTIGGGCTICC
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
719: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 269.6; DB 13;
Pred. No. 2.8e-62;
0; Mismatches 11;
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   organism="Mus musculus"
                                                                                                     /db_xref="taxon:10090"
/clone="K630022E19"
/tissue_type="heart"
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                                     /mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity 95.5%;
Matches 298; Conservative
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Sokazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,T., Osato,N., Saito,R., Suruki,H., Yamanakai,T. Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Marchada,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
J.L., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
,A., Frazer,K.S., Gaaserland,T., Garibold,M., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
,P.A., Maglott,D.R., Multais,L., Marchionni,L., McKenzie,L., Miki,
H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
Pescole,G., Petrovsky,N., Pillai,R., Powin,W.J., Pertea,G.,
Ramachandran,S., Savasi,T., Reed,J.C., Reed,D.J., Semple,C.A., Setou
,M., Shimada,K., Sultana,R., Pohilus,J.U. Qi,D.,
Ramachandran,S., Sandelin,A., Schneider,C., Semple,C.A., Setou
,M., Sakazume,N., Wells,C., Wilming,L.G., Wunshaw,Boris,A., Yanagisawa
,M., Sakazume,N., Sano,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inchin,M., Sakazume,N., Sakai,M., Sanuishi,A., Yoshino,M., Waterston,R., Lander
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura, T., Arakawa,T., Komo,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10); 1617-1630 (2000) RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11); 1757-1771 (2000)
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
                                                                                                            Mus musculus
Eukaryota; Metazoa;
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7

Gaps

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121

2245

239

2305

source FEATURES

Location/Qualifiers

360

420

480

79

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Email: benco-soares@ulowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1790595 The following
repetitive elements were found in this cDNA sequence: 45-167,
Seq primer: M13 Forward.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                            194 GGTTGAGGGTCACCACACATGAGGCCACCACACTGTTCTGGGGGAA---CAGTGGAGAG 138
   181 TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCCTCGACCCCTTTGG 240
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-R-AG1-aal-b-08-0-UI.rl UI-R-AG1 Rattus norvegicus cDNA clone
UI-R-AG1-aal-b-08-0-UI 5', mRNA sequence.
                                                                                                                                                                  289 ---------GTCACATATCATCTATCTGTATATCAATATTCA
                                                                                                                                                                                                                                     301 CATTACGATTCGTAACAGTAGCAAATTACAGGTATGAAATAGCAATGAAATAATTTAT
                                                                                                                                                                                                                                                                                                                                                         GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG
                                                                                                                       241 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 GAAAGCCTTTCAGCTGTTCTGCTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTA 535
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                             332 TTCAGGGTCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGA----
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Coordinated Laboratory for Computational Genomics
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Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
normalized rat heart pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 170-292,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 191.6; DB 12; Length 478; 69.5%; Pred. No. 7.4e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4e-41;
les 80; Indels

    .478
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_LIB=UI-R-DK0
TAG_TISSUE=rat heart pool
                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                         Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG SEQ=ATAAGATAAC"
                                                                                                              >URRIA#DNA/MERI type
Seg primer: M13 Forward
POLYA=Yes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 372; Conservative
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normalized AV canal at 15 dpc library cDNA Librar M.B. Soares Lab Clone distribution: clones will through Research Genetics (www.resgen.com) The fcelements were found in this cDNA sequence: 1-44,
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                                                                                                                                                                                            organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cccrccacrcrrcrrcaradanaacaaca 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                             /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 171;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW251306.1 GI:6594897
EST.
Rattus norvegicus (Norway rat)
                                                                                                                                                   Location/Qualifiers
                                                                                  >POLY A#Simple repeat
Seg primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.3%;
Best Local Similarity 78.4%;
Matches 261; Conservative
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UI-R-BJO-adx-e-05-0-UI.S1 UI-R-BJO Rattus norvegicus cDNA clone
UI-R-BJO-adx-e-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           440
                                                                                                                                                                                                                                                     CAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTA 320
                                                                                                                                                                                                                                                                                                                                       GCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGAAGGTCACCACAACA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 GGAGCCAAGACGCATCGTGGGGGGGAAGACGCAACCTCACCTTCTAGCTCTGCATCC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 TGATTITCTGCTTCTCCTGNGTGGAACCAAGACTGGATCGTTGTCTAGCCCTGCATCT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology,
                                                                                                                                                                                                                                                                                              CTGGAGTCACATATCATCTATCTATATCAAATATTCACATCATGACTCATAACAGTA
                                                                                                                                                                                                                                                                                                                                                                              103 ACACAATTACAGGCATGATGTAGCAATGAATGATTTTTATGGTTGAGGGTCACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGGCCACCACACTGTTCTGGGGGAA----CAGTGGAGAGGAAAGGATTGAGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TTCCATCTGTTCTGCACTCTTCAAAGGGATGTATTCACAGAAAGCCTTTGGTCGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 GCTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTATGTACCAGGTCTGCTTCTTATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITCTGTCCATTCTTCATTCTTCAAAGTGATGTGTTCACAGAAAGCCTTTCAGCTGTTCT
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                  Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
The Newton Road, 4156 MEBRF, Iowa City, IA 52242,
Tel: 119 335 9565
Fax: 319 335 9565
                                                                                                        · 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coordinated Laboratory for Computational Genomics
                                                                                                                                                                    Score 183; DB 10;
Pred. No. 1.6e-38;
0; Mismatches 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                    University of Iowa."
94 c 103 g
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                                                                                                     103 g
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                                                                                                                                                                7.8%;
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                                                                                                                                                                                      Best Local Similarity '... Matches 276; Conservative
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PUBMED
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/db xref="taxxon:10116"
/db xref="taxxon:10116"
/db xref="dault" | /dev adx-e-05-0-UI"
/dab host="dult" | /dev adult" | /dev adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld adult" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab host="buld" | /dab
Library Preparation:
will be available
The following repetitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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UI-R-BJO-adg-f-04-0-UI.sl UI-R-BJO Rattus norvegicus cDNA clone
UI-R-BJO-adg-f-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 ATGGAAACCAGAAGCCCAACAGTTGTCCTTCGATAGTGTCTCTCAGGACAGCCAGGACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   879 ATGAAAACGAGAAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         999 AATGTCTTGTACTGAAGATTCTAGAAACACAATTTGCTGGTTGAACAGCTGAAGTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 GCCAGCAT----ACAAACATAACACCCTAATTAATGCTTCCTCTGGTACTGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        939 AGAACACTAGGAGAGAGAACCCACGAAGGACAAGGTATTAGTGTGTTGGTTTTCAGGGC
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.; 3.3e-35; Indels
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Email: bench-soares@ulowa.edu

The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized ventricle at 13 dpc library CDNA bibrary Preparation:

M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this CDNA sequence: 1-43,
                                                                       EST 04-JUN-1999
100 GCCAGCAT-----ACAAACATAACACCCTAATTAATGCTTCCCTCTGCTACTGACACACTCT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                  AI710529
UI-R-AG1-aal-b-08-0-UI.sl UI-R-AG1 Rattus norvegicus cDNA clone
UI-R-AG1-aal-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
                                                                                                                                                                   1176 CTTCACTCTCTTTCATAAAAAAAAAA 1208
                                                                                                                                                                                              CCTTCACTCTTCTTCATAAAATAAACAAACA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
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Seg primer: M13 Forward
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AI710529.1 GI:5000305
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AI710529/c
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//lab_host="adult"
//lab_host="DH10B (Life Technologies)"
//clone lib="ull"R-B40"
//clone lib="ull"R-B40"
//note="vector: pT710-Pac (Pharmacia) with a modified
//note="vector: pT710-Pac (Pharmacia) with a modified
//note="vector: pT710-Pac (Pharmacia) with a ull-R-B40
library is a subtracted library derived from the UI-R-B40
UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AB1, UI-R-AF1, and
UI-R-AG1 libraries. These libraries represent tissues from
rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
at 16.5 dpc, atrium at 15 dpc, ventricle at 13 dpc. AV
canal at 15 dpc, and ventricle at 13 dpc. The tag is a
string of 5-6 nucleotides present between the Not I site
and the oligo-dT track. The library was constructed as
described by Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGTCTTGTACTGAAGATTCTAGAACACACATTTGCTGGTTGAACAGCTGAAGTGGGGGT 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 AATGTCTCATTCCGAAGGTTCTAGAAACACAGTTTACTGGATGAAGAGGTGAGGGT 161
                           Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                  Email: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                           1 (bases 1 to 511)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                         University of Iowa 375 NEBRP, Iowa City, IA 52242, USA 1319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.3%; Score 171; DB 9; Length 511; 78.4%; Pred. No. 3.3e-35;
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                                                                                                                                                                                                                                                          Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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/clone="UI-R-BJO-adg-f-04-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_TISSUE=ventricle at 13 dpc
TAG_SEQ=CAGCGA"
120 c 113 g 151 t

    511
    forganism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague_Dawley"

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                        Chordata;
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TAG LIB-UI-R-BJO
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                                                 Mammalia; Eutheria;
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    Rattus norvegicus
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ઠે 원 ò 셤 8 a Length 735;

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Query Match 5.6%;
Best Local Similarity 83.6%;
Matches 173; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 735)

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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                               ----CACTAGGAGAGAGAACCCACGAAGGA-----TATCAGTGTGCTGGTTCCAAGGGC
                                                                                                                                                                                                                                          939 AGAACACTAGGAGAGGGGAACCCACGAAGGACAAGGTATTAGTGTTTGGTTTTTCAGGGC
                                                                                                       879 ATGAAAACGAGAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG
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                                                                           Gaps
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AU139209 PLACE1 Homo sapiens CDNA clone PLACE1010155 5', mRNA
                                           Score 167.8; DB 9; Length 370;
Pred. No. 2.2e-34;
0; Mismatches 57; Indeis 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Takao Isogai
Genomics Laboratory
Hellix Research Institute
123-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                       1176 CTTCACTCTCTTTCATAAAAAAAAA 1208
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181 g 156
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1010155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="placenta"
/clone lib="PLACE1"
/note="Vector: pME18SFL;
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human cDNA project
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Matches 259; Conserv
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uu52e68.yl Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:3375590 5' Similar to gb:L35933 Mouse erythrocyte protein 4.2
(MOUSB);, mRNA sequence.
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                                                                                                                                                                                                                                            2225 CCAGCCCTAGCTATATAA-CGGGCTGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGG 2283
                                                                                                                                                                                       88 GTTGGCTCCTAATGGGGGGGGGGGGTTCTTCGGTTCCCAGGTTGGAAGATTATCTCAC 147
                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
MGI:1085194
                                                                                                         28 TCCCCTCCTTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCTCTGA
                                                                                    2105 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGA
                                               Gaps
                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 119.6; DB 10; Length 509; Pred. No. 4e-21;
                                             Indels
Score 131.8; DB 9;
Pred. No. 2.1e-24;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                           2284 TTCATCCACAAGAGAAAAAAAAAAA 2310
                                                                                                                                                                                                                                                                                                                                                 208 TTCCTTC-CACGACAAAAACATACA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:3375590"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE627514.1 GI:9907936
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Unpublished
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Best Local Similarity
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electrophoresis. Vector DNA was prepared from a derivative
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                                                                                                                                                                                                                                                                                                   151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 AACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 AACATGAGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 151; Conserv
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                                                                                                                                                            432 TACT-TICACAGGGTAGGCTATCAGGTATCCTGCATATCAGATATTTACATTATGATTC 374
                                          192 CCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAAC 251
                                                                                                                                       311
                                                                                                                                                                                                                            312 GTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTC 371
                                                                                                                                                                                                                                                      373 CTAACAGTAGCAAATTTATAGTTGTAGCAATGAAATAAAGTTATGGTTGGGGGTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mesea 1 to 538)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                     492 cccracciradaccaciatricicaaccieresesecreaccicirireseses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 bp DNA linear GSS 20-FEB-200
smid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                252 GACCCTTTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTC
    Gaps
    ;;
39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZMO065I13R Mouse 10kb plasmid UUGC1M library Mu
clone_UUGC2M0065113 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: I column: 13
Seg primer: CACACAGGAAACAGCTAATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 538.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0065I13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ804735.1 GI:12965546
                                                                                                                                                                                                                                                                                                                    372 ACCACACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                               313 ACCACACATGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .538
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AZ804735/c
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of pWD42 (gi|473114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ480395 11-236B22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-236B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 TTTACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAAC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 AGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGAAGGTCACCAC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AGTACCAAAATTACAGTTTTGAAGTAGCAATGAATAATTTTTATGGTTGGAGGTCACCAC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter de Jong (pieterage) availability, please contact Pieter de Jong (pieterage) please (bieterage) availability, blease (bloomes may be purchased from ARAPPAR Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 ITCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 TTCTAAGGCAATCTCTCTCAACCTACGGGTTTCGACCCCTTTGGG-----TATCAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 Trcacaggggrcacatatcacatatrcigcargrcagatatracatracagricataac
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Tel: 301 838 0200
Fax: 301 838 0208
Email: hb@cigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 116.2; DB 28; Length 538; 79.9%; Pred. No. 3.5e-20; Live 0; Mismatches 33; Indels 5;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .522
/organism="Homo sapiens"
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/db_xref="GDB:7590285"
/db_xref="taxon:9606"
/clone="RPCI-11-236B22"
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Other GSSs: RPCI-11-236B22.TJ
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AZ290439/c
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COMMENT
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                                                                                                                                                                                                                                         1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT 1597
                                                                                                                                                                                                                                                                                                                  1598 TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAGT 1657
                                                                                                                                                                                                                                                                                                                                                                                         1658 GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tyzo.

Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library and albituty, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 518)
                                                                                                                                                                                                                                                                             202 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT 143
                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                 82 GCATTACTGAATGCTTTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTA 23
Gaps
                                                                                                                                                                                                     7
                                                                                                                                                            Length 522;
                                                                                                                                                                                                   45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other GSSS RPCI-23-449H23.TV
Other GSSS RPCI-23-449H23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                              Score 116; DB 28;
Pred. No. 3.9e-20;
                                                                                                                                                                                                   0; Mismatches
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/organism="Mus musculus"
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/clone="RPCI-23-449H23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1718 TTTAGCTGCAGACATCACTCCA 1739
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/lab_host="DH10B"
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GSS.
                                                                                                                                                                4.9%;
                                                                                                                                                            Query Match
Best Local Similarity 76.79
Matches 155; Conservative
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Class: BAC ends.
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KEYWORDS
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ORGANISM
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JOURNAL
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AZ114168
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Contact: Shaying Inc.
Contact: Shaying Inc.
Contact: Shaying Inc.
Contact: Shaying Inc.
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szlac@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACBAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac.ends/mouse/bac_end_intro.html
/note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
BCORI; Site 2: BCORI; Female C57BL/65 mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
BCORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

94 c 108 g 158 t
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Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 CAGCAGITCICAACCIGGGGGCCICGACCCTITIGGGGGAAICAAACGACCCTITACAGG 264
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 596)
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Other_GSSs: RPCI-23-59G22.TJB
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Best Local Similarity 67.2
Matches 162; Conservative
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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CSTBL60"

/db xref="taxon:10090"

/clone="RPCI-23-59G22"

/sex="Female"

/lab_host="BrOI-23"

/clone lib="RPCI-23"

/looe="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:

/note="Organ: Kidney and/or brain genomic DNA was cloned into the pBACe3.6 vector at the Ecom: Site_Scom: The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

/note="Organ: The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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